

STIC-Biotech/ChemLib

From: Chan, Christina
Sent: Tuesday, February 07, 2006 7:17 PM
To: Basi, Nirmal; STIC-Biotech/ChemLib
Subject: RE: rush search for App. #: 10/036,568

Please ~~rush~~ Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

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FEB - 8 2006
STIC-BIOTECH/ChemLib

-----Original Message-----

From: Basi, Nirmal
Sent: Tuesday, February 07, 2006 7:16 PM
To: Chan, Christina
Subject: rush search for App. #: 10/036,568

Christina I am seeking approval for a RUSH sequence search for this amended case, as indicated below. If approved, could you please forward the search to STIC and cc a copy to me.

Examiner: Nirmal S. Basi
Art Unit 1646
Office: Remsen Building, Room 4D68
Mail Room: Remsen Building, room 4C70.

Sequence search:

App. #: 10/036,568
Result format: Paper.

Title: **NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME**

Inventors: Willson et al

Priority Date: 10/23/1996

Please search:

- i) SEQ ID NO:4
- ii) Polypeptide comprising amino acids 26-426 of SEQ ID NO:4
- iii) Polypeptide comprising amino acids 26-345 of SEQ ID NO:4

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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Search issued, commercial and interference databases.

Thanks,
Nirmal S. Basi

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2006, 22:06:20 ; Search time 35.2833 Seconds
(without alignments)
998.200 Million cell updates/sec

Title: US-10-036-568A-4
Perfect score: 2320
Sequence: 1 MEWPARLCGLWALLLCAGG.....QTKETDSVLIENLKASQ 426

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCRTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2320	100.0	426	2	US-09-688-286D-4
2	2309.5	99.5	427	2	US-08-969-125-9
3	2309.5	99.5	427	2	US-09-545-002-9
4	2309.5	99.5	427	2	US-09-949-016-6094
5	1878	80.9	405	2	US-09-828-995B-50
6	1875.5	80.8	793	2	US-09-313-942-32
7	1875.5	80.8	793	2	US-10-282-162-32
8	1779.5	76.7	784	2	US-09-313-942-30
9	1779.5	76.7	784	2	US-10-282-162-30
10	1769	76.2	322	2	US-09-825-561A-82
11	1696	73.1	424	2	US-09-688-286D-2
12	1265	54.5	233	2	US-09-949-016-8550
13	329	14.2	386	2	US-09-828-995B-61
14	318	13.7	398	1	US-07-757-390-6
15	318	13.7	398	1	US-08-442-282-6
16	318	13.7	398	1	US-08-442-281-6
17	318	13.7	398	1	US-08-939-727-6
18	318	13.7	415	1	US-07-757-390-5
19	318	13.7	415	1	US-08-442-282-5
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22	318	13.7	415	2	US-09-886-319A-23
23	310	13.4	365	2	US-09-828-995B-66
24	304.5	13.1	561	2	US-09-828-995B-72
25	303.5	13.1	561	2	US-09-828-995B-81
26	297	12.8	565	2	US-09-828-995B-75
27	296.5	12.8	420	2	US-09-886-319A-24

28 296.5 12.8 420 2 US-09-949-016-5958 Sequence 5958, Ap
29 296 12.8 318 2 US-09-828-995B-69 Sequence 69, Appl
30 296 12.8 563 2 US-09-828-995B-78 Sequence 78, Appl
31 294.5 12.7 380 1 US-08-609-572-4 Sequence 4, Appl
32 294.5 12.7 380 2 US-08-841-751-4 Sequence 4, Appl
33 294.5 12.7 380 2 US-08-846-340-4 Sequence 4, Appl
34 294.5 12.7 380 2 US-08-846-344-4 Sequence 4, Appl
35 294.5 12.7 380 2 US-09-301-808-4 Sequence 13, Appl
36 294.5 12.7 420 1 US-07-757-390-13 Sequence 13, Appl
37 294.5 12.7 420 1 US-08-442-282-13 Sequence 13, Appl
38 294.5 12.7 420 1 US-08-442-281-13 Sequence 13, Appl
39 294.5 12.7 420 1 US-08-939-727-13 Sequence 8614, Ap
40 293.5 12.7 427 2 US-09-949-016-8614 Sequence 8620, Ap
41 293.5 12.7 383 1 US-08-609-572-2 Sequence 2, Appl
42 287.5 12.4 383 1 US-08-841-751-2 Sequence 2, Appl
43 287.5 12.4 383 2 US-08-846-340-2 Sequence 2, Appl
44 287.5 12.4 383 2 US-08-846-344-2 Sequence 2, Appl
45 287.5 12.4 383 2 US-08-846-344-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-688-286D-4

; Sequence 4, Application US/09688286D

; Patent No. 6911530

; GENERAL INFORMATION:

; APPLICANT: Willson, Tracey

; APPLICANT: Nicola, Nicos

; APPLICANT: Hilton, Douglas

; APPLICANT: Metcalf, Donald

; APPLICANT: Zhang, Jian

; TITLE OF INVENTION: A novel haemopoietin receptor and genetic sequences encoding same

; FILE REFERENCE: 23199-215

; CURRENT APPLICATION NUMBER: US/09/688,286D

; CURRENT FILING DATE: 2003-07-10

; PRIOR APPLICATION NUMBER: AU PN6135

; PRIOR FILING DATE: 1995-10-23

; PRIOR APPLICATION NUMBER: AU PN276

; PRIOR FILING DATE: 1995-12-22

; PRIOR APPLICATION NUMBER: AU PP2208

; PRIOR FILING DATE: 1996-09-09

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 4

; LENGTH: 426

; TYPE: PRT

; ORGANISM: human

US-09-688-286D-4

Query Match 100.0%; Score 2320; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 5.2e-220;
Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEWPARLCGLWALLLCAGGGGGGAGTETQPPVTNLSVSVNLCVITWNPPEGASSN 60
DB 1 MEWPARLCGLWALLLCAGGGGGGAGTETQPPVTNLSVSVNLCVITWNPPEGASSN 60
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DB 61 CSLWYFHFPGDKQDKKIAPETRRSIEVPLNERICLVQVSGQCSSTNESEKPSILVEKICSP 120
QY 121 EGDPSAVTELQCIWHNLSYMKCSWLPGRNTSPDNTYLYWHRSLKTHQENIFREG 180
DB 121 EGDPSAVTELQCIWHNLSYMKCSWLPGRNTSPDNTYLYWHRSLKTHQENIFREG 180
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DB 181 YFGCSFDLTKVQSSFEQHSQIWMKDNAGKIKPSNIVPLTSRVKPDPPHINKLSFHD 240
QY 241 DLVYQWENPQNTFISRLCLFYEVVNSQETHTNVFVYQEAKECNPEPERNVENTSCFMPVFG 300

Db 241 DLYVQWENPQNFISRCLFYEVEVNNSTQETHNVFVQEAECNPEPERNVENTSCFMVPG 300
Qy 301 VLPDPTLNTVIRVKTNKLKYEDDDKLSNWSQMSIGKKNSTLYITMLLIVPVIAGAI 360
Db 301 VLPDPTLNTVIRVKTNKLKYEDDDKLSNWSQMSIGKKNSTLYITMLLIVPVIAGAI 360
Qy 361 VLLLYLRLKLIIFPPPIPDGKIFKEMFGQNDNDDLHWKKYDIYEKQTEETSDSVLLIEN 420
Db 361 VLLLYLRLKLIIFPPPIPDGKIFKEMFGQNDNDDLHWKKYDIYEKQTEETSDSVLLIEN 420
Qy 421 LKXASQ 426
Db 421 LKXASQ 426

RESULT 2
US-08-969-125-9
; Sequence 9, Application US/08969125B
; Patent No. 6143871
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, JEAN-YVES
; GAUCHAT, JEAN-FRANCOIS
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,125B
; FILING DATE: 12-No. 6143871-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9625899.1
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 427 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-969-125-9

Query Match 99.5%; Score 2309.5; DB 2; Length 427;
Best Local Similarity 99.8%; Pred. No. 5.6e-219;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MEWPARLCGLWALLCAGGGGGGGG-APTQTPVNLNLSVSVENLCTVIWTNPPPGASS 59
Db 1 MEWPARLCGLWALLCAGGGGGGGG-APTQTPVNLNLSVSVENLCTVIWTNPPPGASS 60
Qy 60 NCSLWTFSHFGDKQDKKIAPTRRSIEVPLNERICLVQVGCSTNSEKPSILVEKICIS 119
Db 61 NCSLWTFSHFGDKQDKKIAPTRRSIEVPLNERICLVQVGCSTNSEKPSILVEKICIS 120
Qy 120 PEGDPESAVTELOCINHLNLSYMKCSWLPGRNTSPDNTYTLTYWHSRLEKIHQCNIFREG 179

Db 121 PEGDPESAVTELOCINHLNLSYMKCSWLPGRNTSPDNTYTLTYWHSRLEKIHQCNIFREG 180
Qy 180 QYFGCSFDLTQVXDSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHN 239
Db 181 QYFGCSFDLTQVXDSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHN 240
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Db 241 DDLYVQWENPQNFISRCLFYEVEVNNSTQETHNVFVQEAECNPEPERNVENTSCFMVPG 300
Qy 300 GVLPTLNTVIRVKTNKLKYEDDDKLSNWSQMSIGKKNSTLYITMLLIVPVIAGAI 359
Db 301 GVLPTLNTVIRVKTNKLKYEDDDKLSNWSQMSIGKKNSTLYITMLLIVPVIAGAI 360
Qy 360 IVLLLYLRLKLIIFPPPIPDGKIFKEMFGQNDNDDLHWKKYDIYEKQTEETSDSVLLIE 419
Db 361 IVLLLYLRLKLIIFPPPIPDGKIFKEMFGQNDNDDLHWKKYDIYEKQTEETSDSVLLIE 420
Qy 420 NLKXASQ 426
Db 421 NLKXASQ 427

RESULT 3
US-09-545-002-9
; Sequence 9, Application US/09545002
; Patent No. 6743604
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, JEAN-YVES
; GAUCHAT, JEAN-FRANCOIS
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/545,002
; FILING DATE: 12-No. 6743604-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,125
; FILING DATE: 12-No. 6743604-1997
; APPLICATION NUMBER: GB 9625899.1
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 427 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-545-002-9

Query Match 99.5%; Score 2309.5; DB 2; Length 427;
Best Local Similarity 99.8%; Pred. No. 5.6e-219;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db 1 MWPRLCGLWALLCAGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTVNPPGASS 60
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Db 61 NCSLWYFSHFGDKQDKKIAPETRSIEVPLNERICLVQVSCQSTNESEKPSILVEKICSP 120
QY 120 PGDPESAVENTELQCIWHNLSYMKCSWLPGRNTSPDNTYLYWHSRSLKIHQECENIFREG 179
Db 121 PGDPESAVENTELQCIWHNLSYMKCSWLPGRNTSPDNTYLYWHSRSLKIHQECENIFREG 180
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Db 181 QYFGCSFDLTAKVQDSSFEQHSVQIMVKDNAGKIKPSFNIPLTSRVKPDPPHIIKXLSFHN 240
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Db 241 DDLYVQWENPQNFISRCIFYEVVNNSTQTHNVFYVQEAECENPEFERNVENTSCFMPV 300
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Db 301 GVLDDTLNTVIRVKTNKLKCYEDDDKLSNWSQMSIGKRNSTLYITMLLIVPVIVAGAI 360
QY 360 IVLLLYLKLKLIIFPPIDPGKIPKEMFGQNDTLLHWKYDIYEKQKETSVDVLLIE 419
Db 361 IVLLLYLKLKLIIFPPIDPGKIPKEMFGQNDTLLHWKYDIYEKQKETSVDVLLIE 420
QY 420 NLKQASQ 426
Db 421 NLKQASQ 427
RESULT 4
US-09-949-016-6094
; Sequence 6094, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6094
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6094
Query Match 99.5%; Score 2309.5; DB 2; Length 427;
Best Local Similarity 99.8%; Pred. No. 5.6e-219;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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Db 1 MWPRLCGLWALLCAGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTVNPPGASS 60
QY 60 NCSLWYFSHFGDKQDKKIAPETRSIEVPLNERICLVQVSCQSTNESEKPSILVEKICSP 119
Db 61 NCSLWYFSHFGDKQDKKIAPETRSIEVPLNERICLVQVSCQSTNESEKPSILVEKICSP 120
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Db 121 PGDPESAVENTELQCIWHNLSYMKCSWLPGRNTSPDNTYLYWHSRSLKIHQECENIFREG 180
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Db 181 QYFGCSFDLTAKVQDSSFEQHSVQIMVKDNAGKIKPSFNIPLTSRVKPDPPHIIKXLSFHN 240
QY 240 DDLYVQWENPQNFISRCIFYEVVNNSTQTHNVFYVQEAECENPEFERNVENTSCFMPV 299
Db 241 DDLYVQWENPQNFISRCIFYEVVNNSTQTHNVFYVQEAECENPEFERNVENTSCFMPV 300
QY 300 GVLDDTLNTVIRVKTNKLKCYEDDDKLSNWSQMSIGKRNSTLYITMLLIVPVIVAGAI 359
Db 301 GVLDDTLNTVIRVKTNKLKCYEDDDKLSNWSQMSIGKRNSTLYITMLLIVPVIVAGAI 360
QY 360 IVLLLYLKLKLIIFPPIDPGKIPKEMFGQNDTLLHWKYDIYEKQKETSVDVLLIE 419
Db 361 IVLLLYLKLKLIIFPPIDPGKIPKEMFGQNDTLLHWKYDIYEKQKETSVDVLLIE 420
QY 420 NLKQASQ 426
Db 421 NLKQASQ 427
RESULT 5
US-09-828-995B-50
; Sequence 50, Application US/09828995B
; Patent No. 6703360
; GENERAL INFORMATION:
; APPLICANT: Heska Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/09/828,995B
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-828-995B-50
Query Match 80.9%; Score 1878; DB 2; Length 405;
Best Local Similarity 85.2%; Pred. No. 1.9e-176;
Matches 345; Conservative 24; Mismatches 36; Indels 0; Gaps 0;
QY 22 GGGGAPTETQPPVTNLSVSVENLCTVIWTVNPPGASNCSLWYFSHFGDKQDKKIAPET 81
Db 1 GGVAAPTETQPPVTNLSVSVENLCTVIWTVNPPGASPNCTLYFSDNDKQDKKIAPET 60
QY 82 RRSIEVPLNERICLVQVSCQSTNESEKPSILVEKICSPPEGDPESAVENTELQCIWHNLSY 141
Db 61 HRSKEVPLNERICLVQVSCQSTNESEKPSILVEKICSPPEGDPESAVENTELQCIWHNLSY 120
QY 142 KCSLWLPGRNTSPDNTYLYWHSRSLKIHQECENIFREGQYFCGSDLTAKVQDSSFEQHSV 201
Db 121 KCTLWLPGRNTSPDNTYLYWHSRSLKIHQECENIFREGQYFCGSDLTAKVQDSSFEQHSV 180
QY 202 QIMVKDNAGKIKPSFNIPLTSRVKPDPPHIIKXLSFHNDDLYVQWENPQNFISRCIFYEV 261
Db 181 QIMVKDNARKIRPSFNIPLTSRVKPDPPHIIKXLSFHNDDLYVQWENPQNFISRCIFYEV 240
QY 262 EVNNSQTHNVFYVQEAECENPEFERNVENTSCFMPVGLVDDTLNTVIRVKTNKLKCYE 321
Db 241 EVNNSQTHNDIFYVEBAKCCNSEFEGNLEGTCFMPVGLVDDTLNTVIRVKTNKLKCYE 300
QY 322 DDKLSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLLYLKLKLIIFPPIDPG 391
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Db 361 KIFKEMFGDNDTDLHWKDYIYEKQKKESTDSVLIENLKASQ 405

RESULT 6
US-09-313-942-32
; Sequence 32, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-32

Query Match 80.8%; Score 1875.5; DB 2; Length 793;
Best Local Similarity 99.4%; Pred. No. 9.1e-176;
Matches 341; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MWPARLCGLWALLLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 59
Db 1 MWPARLCGLWALLLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 60

QY 60 NCSLWYFSHFQDKQDKKIAPETRRSIEVPLNERICLVQVSGQCSQSTNESEKPSILVEKCI 119
Db 61 NCSLWYFSHFQDKQDKKIAPETRRSIEVPLNERICLVQVSGQCSQSTNESEKPSILVEKCI 120

QY 120 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYLYYWHRSLEKIHQENIFREG 179
Db 121 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYLYYWHRSLEKIHQENIFREG 180

QY 180 QYFGCSFDLTVKVDSSEFQHSVQIMVKDNAGKIKPSFNIPLTSRVKPDPPHIKNLSFHN 239
Db 181 QYFGCSFDLTVKVDSSEFQHSVQIMVKDNAGKIKPSFNIPLTSRVKPDPPHIKNLSFHN 240

QY 240 DDLVQWENPQNFISRCLFYEVEVNNSTQETHNVFYVQBAKCNPFERNVENTSCFMVP 299
Db 241 DDLVQWENPQNFISRCLFYEVEVNNSTQETHNVFYVQBAKCNPFERNVENTSCFMVP 300

QY 300 GVLPTDLTNTVIRVKTNKLCEYDDKLSNWSQMSIGKKRNST 342
Db 301 GVLPTDLTNTVIRVKTNKLCEYDDKLSNWSQMSIGKKRNST 343

RESULT 8
US-09-313-942-30
; Sequence 30, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-30

Query Match 76.7%; Score 1779.5; DB 2; Length 784;
Best Local Similarity 90.4%; Pred. No. 2.6e-166;
Matches 328; Conservative 5; Mismatches 15; Indels 15; Gaps 2;

QY 20 GGGGGAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFQDKQDKKIAP 79
Db 233 GGGGGAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFQDKQDKKIAP 292

QY 80 ETRRSIEVPLNERICLVQVSGQCSQSTNESEKPSILVEKCI 139
Db 293 ETRRSIEVPLNERICLVQVSGQCSQSTNESEKPSILVEKCI 352

QY 140 YMKCSWLPGRNTSPDNTYLYYWHRSLEKIHQENIFREGQYFGCSFDLTVKVDSSEFQHSVQIMVKDNAGKIKPSFNIPLTSRVKPDPPHIKNLSFHN 199
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Db 353 YMKCSWLPGRNTSPDNTYLYWHSLEKIHQCENIFREGQYFGCSFDLTVKVDSSEFQH 412
Qy 200 SVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLYQWENPQNFISRCIFY 259
Db 413 SVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLYQWENPQNFISRCIFY 472
Qy 260 EVEVNSQTEHNVFYVQEAKECPENPERNVENTSCFMVPGVLPDTLNTRVIRVKTNKLK 319
Db 473 EVEVNSQTEHNVFYVQEAKECPENPERNVENTSCFMVPGVLPDTLNTRVIRVKTNKLK 532
Qy 320 YEDDKLWSNWSQEMSIGKGRNST----LYITMLLIVPVIVAGAIIVLLLYLKRKLIIFFP 375
Db 533 YEDDKLWSNWSQEMSIGKGRNSTTGDKTHTCCPPCAPELLGSP-----SVFLFP 581
Qy 376 PIP 378
Db 582 PKP 584

RESULT 9
US-10-282-162-30
; Sequence 30, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE OF INVENTION: AND USING
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-30

Query Match 76.7%; Score 1779.5; DB 2; Length 784;
Best Local Similarity 90.4%; Pred. No. 2.6e-166;
Matches 328; Conservative 5; Mismatches 15; Indels 15; Gaps 2;

Qy 20 GGGGGGAPTETPTPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSGHFGDKQDKKIAP 79
Db 233 GGGGGAAPTETPTPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSGHFGDKQDKKIAP 292
Qy 80 ETRRSIEVPLNERICLVQVGSQCTNSESEKPSILVEKICISPPGDPESAATELQCIWHNLS 139
Db 293 ETRRSIEVPLNERICLVQVGSQCTNSESEKPSILVEKICISPPGDPESAATELQCIWHNLS 352
Qy 140 YMKCSWLPGRNTSPDNTYLYWHSLEKIHQCENIFREGQYFGCSFDLTVKVDSSEFQH 199
Db 353 YMKCSWLPGRNTSPDNTYLYWHSLEKIHQCENIFREGQYFGCSFDLTVKVDSSEFQH 412
Qy 200 SVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLYQWENPQNFISRCIFY 259
Db 413 SVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLYQWENPQNFISRCIFY 472
Qy 260 EVEVNSQTEHNVFYVQEAKECPENPERNVENTSCFMVPGVLPDTLNTRVIRVKTNKLK 319
Db 473 EVEVNSQTEHNVFYVQEAKECPENPERNVENTSCFMVPGVLPDTLNTRVIRVKTNKLK 532
Qy 320 YEDDKLWSNWSQEMSIGKGRNST----LYITMLLIVPVIVAGAIIVLLLYLKRKLIIFFP 375
Db 533 YEDDKLWSNWSQEMSIGKGRNSTTGDKTHTCCPPCAPELLGSP-----SVFLFP 581
Qy 376 PIP 378
Db 582 PKP 584
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Db 582 PKP 584

RESULT 10
US-09-825-561A-82
; Sequence 82, Application US/09825561A
; Patent No. 6777539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. 6777539ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-82

Query Match 76.2%; Score 1769; DB 2; Length 322;
Best Local Similarity 99.7%; Pred. No. 7.4e-166;
Matches 321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 GGGGGAPTETPTPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSGHFGDKQDKKIAP 80
Db 1 GGGGAAPTETPTPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSGHFGDKQDKKIAP 60
Qy 81 TRRSIEVPLNERICLVQVGSQCTNSESEKPSILVEKICISPPGDPESAATELQCIWHNLS 140
Db 61 TRRSIEVPLNERICLVQVGSQCTNSESEKPSILVEKICISPPGDPESAATELQCIWHNLS 120
Qy 141 MKCSWLPGRNTSPDNTYLYWHSLEKIHQCENIFREGQYFGCSFDLTVKVDSSEFQH 200
Db 121 MKCSWLPGRNTSPDNTYLYWHSLEKIHQCENIFREGQYFGCSFDLTVKVDSSEFQH 180
Qy 201 VQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLYQWENPQNFISRCIFY 260
Db 181 VQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLYQWENPQNFISRCIFY 240
Qy 261 VEVNSQTEHNVFYVQEAKECPENPERNVENTSCFMVPGVLPDTLNTRVIRVKTNKLK 320
Db 241 VEVNSQTEHNVFYVQEAKECPENPERNVENTSCFMVPGVLPDTLNTRVIRVKTNKLK 300
Qy 321 EDDKLWSNWSQEMSIGKGRNST 342
Db 301 EDDKLWSNWSQEMSIGKGRNST 322

RESULT 11
US-09-688-286D-2
; Sequence 2, Application US/09688286D
; Patent No. 6911530
; GENERAL INFORMATION:
; APPLICANT: Willson, Tracey
; APPLICANT: Nicola, Nicos
; APPLICANT: Hilton, Douglas
; APPLICANT: Metcalf, Donald
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: A novel haemopoietin receptor and genetic sequences encoding same
; FILE REFERENCE: 23199-215
; CURRENT APPLICATION NUMBER: US/09/688,286D
; CURRENT FILING DATE: 2003-07-10
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; PRIOR APPLICATION NUMBER: AU PN6135
; PRIOR FILING DATE: 1995-10-23
; PRIOR APPLICATION NUMBER: AU PN7276
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: AU PP2208
; PRIOR FILING DATE: 1996-09-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-688-286D-2

Query Match      73.1%; Score 1696; DB 2; Length 424;
Best Local Similarity 74.8%; Pred. No. 1.8e-158;
Matches 318; Conservative 40; Mismatches 65; Indels 2; Gaps 2;

Qy 1 MWPRLCGIWLALLCAGGGGGGAPTETQPPVTNLSVVENLCTVIWTWNPPEGASN 60
Db 1 MARPALGELLVLLLTATVGVAAA--TEVQPPVTNLSVVENLCTIIWTWSPPEGASN 59
Qy 61 CSLWYFSHFQDKQDKKIAPETRRSIEVPLNERICLVGSCSTNESEKPSILVEKCI 120
Db 60 CTLYFSHFDDQDKKIAPETRRKEELPLDEKICLVGSCSANESEKPSPLVKKCLSP 119
Qy 121 EGPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTNLYWHRSLKIHQCNIFREGQ 180
Db 120 EGPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTNLYWHRSLKIHQCNIFREGQ 179
Qy 181 YFGCSPLTKVQSSFEQHSQVIMVKDNAGKIPSNIVPLTSRVKPDPPHINKNLSFND 240
Db 180 HIACSFKLTIV--SPFSHQNVQIMVKDNAGKIPSCKIVSLTSVVKPDPPHINKNLS 238
Qy 241 DLVQWENPQNFISRCILFYEVEVNNSTQETHNVFYVQAKCENPEFERNVENTSCFMV 300
Db 239 ALLVQKNPQNFISRCILFYEVEVNNSTQETHNVFYVQAKCENPEFERNVENTSCFMV 298
Qy 301 VLPDTLTVIRVTKNKLCEYDDKLSNWSQESIGKGRNSTLYITMLLVIPVIVAGAI 360
Db 299 VLADAVTVRVVTKNKLCEYDDKLSNWSQESIGKGRNSTLYITMLLVIPVIVAVI 358
Qy 361 VLLLYLKLKLIIFPPPIPDGKIFKEMFGQNDTLLHWKKYDIYEKOTKEETDSVLLIEN 420
Db 359 ILFLYLRKLIIFPPPIPDGKIFKEMFGQNDTLLHWKKYDIYEKOTKEETDSVLLIEN 418
Qy 421 LKKAAS 425
Db 419 LKKAAS 423

RESULT 12
US-09-949-016-8550
; Sequence 8550; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8550
; LENGTH: 233
; TYPE: PRT
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; ORGANISM: Human
US-09-949-016-8550

Query Match      54.5%; Score 1265; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 2.3e-116;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 76 KIAPETRRSIEVPLNERICLVGSCSTNESEKPSILVEKCI 135
Db 1 KIAPETRRSIEVPLNERICLVGSCSTNESEKPSILVEKCI 60
Qy 136 HNLNLSYMKCSWLPGRNTSPDNTNLYWHRSLKIHQCNIFREGQFGCSFDLT 195
Db 61 HNLNLSYMKCSWLPGRNTSPDNTNLYWHRSLKIHQCNIFREGQFGCSFDLT 120
Qy 196 FEQHSQVIMVKDNAGKIPSNIVPLTSRVKPDPPHINKNLSFNDLIVQWENPQNFIS 255
Db 121 FEQHSQVIMVKDNAGKIPSNIVPLTSRVKPDPPHINKNLSFNDLIVQWENPQNFIS 180
Qy 256 CLFYEVEVNNSTQETHNVFYVQAKCENPEFERNVENTSCFMV 306
Db 181 CLFYEVEVNNSTQETHNVFYVQAKCENPEFERNVENTSCFMV 231

RESULT 13
US-09-828-995B-61
; Sequence 61; Application US/09828995B
; Patent No. 6703360
; GENERAL INFORMATION:
; APPLICANT: Heskia Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13 R
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/09/828,995B
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-828-995B-61

Query Match      14.2%; Score 329; DB 2; Length 386;
Best Local Similarity 26.3%; Pred. No. 9.9e-24;
Matches 109; Conservative 62; Mismatches 171; Indels 72; Gaps 19;

Qy 10 LWALLLCAGGGGGGAPTETQPPVTNLSVVENLCTVIWTWNP--EGASSNCSLWY-- 65
Db 11 LYTLLVCTAFGSMLSNAEIKVNPQDFEIVDPCVLGVLISLQWQPLFPDFNFKECTIEVL 70
Qy 66 -FSHFGDKQDKKIAP-----ETRRSIEVPLNERICLVGSCSTNESEKPSILVEK 115
Db 71 KYRNIDSNNWKTITKNLHYKDGFDLKNKGIKAKINTLL----PAQC--TNGSEVRSSWAET 125
Qy 116 CI--SPPEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTNLYWHRSLKIHQCN 174
Db 126 TYWTSFGNRETKIQDMDCVYINWQYLVCWSKFGMGVHFDNTQLFWYGLDHSACSTD 185
Qy 175 IFR--EGQYFGCSFDLTAKVQSSFEQHSQVIMVKDNAGKIPSNIVPLTSRVKPDPPH 233
Db 186 YIKVGNKNGCRPPY--LESSDYKDFYICVNGSESEQPIRPSYFIQQLQIVKMPDPYL 243
Qy 234 NLSFHN--DDLIVQWENPQNF--SRCLFYEVEVNNSTQETHNVFYVQAKCENPEFERN 289
Db 244 SLTVKNSSEINKWNPKGPIPAKCFIYEIETEDGTWVTTV-----ENEIQ 292
Qy 290 VENTS-----CFMVPGVLPDTLTVIRVTKNKLCEYDDKLSNWSQESIGK--KRN 340
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Db 293 ITRSNBSQKLCFLV-----RSKNYIC-SDDGWSEMSDEQCMKGDIWKET 338
Qy 341 STLVTMLLIYVIVAGAIIVLLYLKR--IKIIFPPIDPPGKIFKEMFGDQON 392
Db 339 LVFELIPPAFVSIFVL-VITCLLYKQKALLKTIHTK-----KEVFSHOD 383

RESULT 14
US-07-757-390-6
; Sequence 6, Application US/07757390
; Patent No. 5453491
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tominaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/757,390
; FILING DATE: 19910910
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Lealie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-757-390-6

Query Match 13.7%; Score 318; DB 1; Length 398;
Best Local Similarity 23.9%; Pred. No. 1.3e-22;
Matches 97; Conservative 74; Mismatches 179; Indels 56; Gaps 14;

Qy 32 PPVTNLSVSVENLCTVIWTPN-PEGASNSCLWTFSSH-GDKQDKKIAPETRRSIEVPL 89
Db 12 PPV-NFTIKATGLAQLVLLHWDNPQEQRHVDLEYHVKNAPQDEYDTRKTESKCVTPL 70
Qy 90 NERICLVGSQCSTNESEKPSILVEKICSPPEGDPDESATVTELCIWHNL----- 138
Db 71 HEGFAASVRTILKSHSTTLASSWSAELKAPPGSGTSTNLTCTTHTVSSHTLHPYQ 130
Qy 139 SYMKCSWLPGRNTSPDTNLYYHRSLEKIHQENIFRE--GOYFGCSFDLTWKVDGSF 196
Db 131 VSLRCTLWVGKADPEDTQFLYRFGVLTE--KCQEYSDALNRNATWACHPFTFINSGKF 188
Qy 197 EQHSVQIMVKDAGKIKPSFNIVPLTSRVKPPPHIKNLSFNDDLYQWENPQN-FISR 255
Db 189 EQLAVHINGSKRAAIKPPDQLFSLAIDQVNPRTVTEIESNSLIYQWEKPLSAFPDH 248
Qy 256 CLFYEVENVNSQTETHNVFYQAEKCNPEFERNVENTSCFMVPGVLPTLNTVIRVKT 315

Db 249 CFNYELKIYNTKNG-----HIQEKLIANKFISKIDDVSTY-----SIQVRAAV 292
Qy 316 NKLCYEDDDKLWSNQBSQMSIGKRNSTLYITMLLIVPVIAGAIIVLLLYLKRLLKII-- 372
Db 293 SSPCRMPGR-WGEWSQFIYVGKERKS-LVEWHLLIVP---TAACFVLLISLCRVCHELW 347
Qy 373 --IPFPPIPDGKIPKEMFGDQNDLTHWKKYDIYEKQTKETSDSV 416
Db 348 TRLPPVPAPKSNIKDL-----PVTVEYKPSNETKIEVW 382

RESULT 15
US-08-442-282-6
; Sequence 6, Application US/08442282
; Patent No. 5760204
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tominaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,282
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Lealie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-442-282-6

Query Match 13.7%; Score 318; DB 1; Length 398;
Best Local Similarity 23.9%; Pred. No. 1.3e-22;
Matches 97; Conservative 74; Mismatches 179; Indels 56; Gaps 14;

Qy 32 PPVTNLSVSVENLCTVIWTPN-PEGASNSCLWTFSSH-GDKQDKKIAPETRRSIEVPL 89
Db 12 PPV-NFTIKATGLAQLVLLHWDNPQEQRHVDLEYHVKNAPQDEYDTRKTESKCVTPL 70
Qy 90 NERICLVGSQCSTNESEKPSILVEKICSPPEGDPDESATVTELCIWHNL----- 138
Db 71 HEGFAASVRTILKSHSTTLASSWSAELKAPPGSGTSTNLTCTTHTVSSHTLHPYQ 130
Qy 139 SYMKCSWLPGRNTSPDTNLYYHRSLEKIHQENIFRE--GOYFGCSFDLTWKVDGSF 196

Db 131 VSLRCTWLVGKAPEDTQYFLYYRFGVLTB--KCQEYSRDALNRENTACWFPRTFINSKGF 188
QY 197 EQHSVQIMVNDNAGKIKPSPNIVPLTSRVKDPDPHKNLSFHNDLLYQWENPON-FISR 255
Db 189 EQLAVHINGSKRAAIKPPDQLFSLAIDQVNPVRNVTVIEGNSLYIQWEKPLSAPPDH 248
QY 256 CLFYEVEVNNSTETHNVFYQEAACENPFRNVENTSCFMVPGVLPDTLNTVIRVKT 315
Db 249 CFNYELKIYNTKNG-----HIQKEKLIANKFISKIDDVSTY-----SIQVRAAV 292
QY 316 NKLCYEDDKLWSNWSQEMSIGKRNSTLYITMLLIVFVIVAGAIIVLLLYLKLKII--- 372
Db 293 SSPCRMGR-WGEWSQIYVGKERKS-LVEWHLIVLP---TAACFVLLIFSLICRVCHLW 347
QY 373 --JFPPIPDGKIFKEMFGQNDTLHWKKYDIYEKOTKEETDSVV 416
Db 348 TRLFPVPVPAPKSNIKDL-----PVTBYEKPSNETKIEW 382

Search completed: February 8, 2006, 22:10:43
Job time : 36.2833 secs

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OM protein - protein search, using sw model

Run on: February 8, 2006, 21:52:58 ; Search time 131.105 Seconds
(without alignments)
1427.670 Million cell updates/sec

Title: US-10-036-568A-4
Perfect score: 2320
Sequence: 1 MEWPARLCGLWALLCAGGG.....QTKETDVSVLINLKKASQ 426

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 21: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *
9: geneseqp2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2320	100.0	426	AAW09822	Human int
2	2309.5	99.5	427	AAW24973	Human int
3	2309.5	99.5	427	AAB19807	Human int
4	2309.5	99.5	427	ADL171812	Human int
5	2309.5	99.5	427	ADL182843	Human PRO
6	2309.5	99.5	427	ADN04504	Antipsori
7	2309.5	99.5	427	ADN62575	Human int
8	2309.5	99.5	427	ADN862241	Tumour-as
9	2303.5	99.3	427	ADL171813	Human int
10	2302.5	99.2	427	ADL17835	Human IL-
11	2302.5	99.2	427	ADL171814	Human int
12	2296.5	99.0	427	AAB19808	Human int
13	2230.5	96.1	414	ADX97531	Pancreat
14	1878	80.9	405	AAU69132	Canine in
15	1875.5	80.8	793	AAU92208	IL-13/IL-
16	1875.5	80.8	793	ABW02181	Human IL-
17	1784.5	76.9	664	ADL17841	Chimeric
18	1779.5	76.7	784	AAU92207	IL-13/IL-
19	1779.5	76.7	784	ABW02180	Human IL-
20	1769	76.2	322	AAE13745	Human sol
21	1714	73.9	426	AAW09821	Mouse int
22	1696	73.1	424	ADX97888	Murine IL
23	1536	66.2	286	AAB90678	Human DA1
24	942	40.6	177	AAW58987	Homo sapi

25	465	20.0	134	8	ADP84617	Human bre
26	463	20.0	172	8	ADP84616	Human bre
27	463	20.0	226	8	ADQ65618	Novel hum
28	414.5	17.9	82	8	ADO26844	Human rec
29	329	14.2	386	4	AAU69135	Canine in
30	318	13.7	398	2	AAU69136	Sequence
31	318	13.7	415	2	AAU69137	Sequence
32	318	13.7	415	2	AAU69138	Sequence
33	318	13.7	415	2	AAU69139	Sequence
34	310	13.4	365	4	AAU69136	Canine in
35	304.5	13.1	561	4	AAU69137	Canine in
36	303.5	13.1	561	4	AAU69141	Canine IL
37	302	13.0	372	2	AAU66616	Celebus m
38	297	12.8	565	4	AAU69139	Canine IL
39	296.5	12.8	420	5	ADZ58698	Human IL-
40	296.5	12.8	421	2	AAU25064	Human IL-
41	296	12.8	318	4	AAU69137	Canine IL
42	296	12.8	563	4	AAU69140	Canine IL
43	294.5	12.7	380	2	AAW36613	Human Dcy
44	294.5	12.7	380	2	AAW35295	Human IL-
45	294.5	12.7	380	2	AAW24972	Human int

ALIGNMENTS

RESULT 1
AAW09822
ID AAW09822 standard; protein; 426 AA.
XX
XX AAW09822;
AC
XX
DT 15-JUL-1997 (first entry)
XX
DE Human interleukin-12 receptor alpha chain NR4.
XX
XX NR4; haemoprotein receptor; interleukin-13 receptor; IL-13; cytokine;
XX
XX allergy; asthma; therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..27
FT /label= Sig_peptide
FT Protein 28..426
FT /label= Mat_protein
FT Domain 28..118
FT /label= Extracellular domain
FT /note= "Ig-like domain"
FT Modified-site 36
FT /label= N-glycosylation site
FT Modified-site 104
FT /label= N-glycosylation_site
FT Domain 119..342
FT /label= Haemoreceptor_receptor-domain
FT Modified-site 137
FT /label= N-glycosylation site
FT Region 326..330
FT /label= WSDWS_motif
FT Domain 343..366
FT /label= Transmembrane_domain
FT Domain 367..426
FT /label= Cytoplasmic_tail
XX
XX WO9715663-A1.
XX
XX 01-MAY-1997.
XX
XX 23-OCT-1996; 96WO-AU000668.
XX
XX 23-OCT-1995; 95AU-00006135.
XX
XX 22-DEC-1995; 95AU-00007276.
XX
XX 09-SEP-1996; 96AU-00002208.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.
PA Willson T, Nicola NA, Hilton DJ, Metcalf D, Zhang JG;
XX WPI; 1997-259018/23.
XX N-PSDB; AAT66165.
DR DNA encoding animal haemopoietin receptor which interacts with
XX interleukin-13 - useful to treat asthma, allergy or condition exacerbated
PT by IGE production.
PT Claim 5; Page 52-54; 93pp; English.
PS Novel mouse and human haemoprotein receptors (AAW09821 and AAW09822),
XX designated NR4, comprise the interleukin-13 (IL-13) receptor alpha-chain.
CC The human NR4 amino acid sequence was deduced from a composite DNA
CC sequence (AAT66165) derived from bone marrow cDNA clones. Recombinant
CC NR4, or fusion proteins including NR4, can be produced in transformed
CC host cells. The receptor molecules and their components are useful in the
CC development of a range of agonists, antagonists, therapeutics and
CC diagnostic reagents based on ligand interaction with its receptor, esp.
CC for the development of cpds. capable of modulating the activity of IL-13
CC and related cytokines such as interleukin-4 for the treatment of allergy,
CC asthma and other conditions relating to IGE
XX
SQ Sequence 426 AA;
Query Match 100.0%; Score 2320; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 4.4e-212;
Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEWPARGLWALLLCAGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWNPPEGASSN 60
DB 1 MEWPARGLWALLLCAGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWNPPEGASSN 60
QY 61 CSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLVGSGCSTNESEKPSILVEKICISP 120
DB 61 CSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLVGSGCSTNESEKPSILVEKICISP 120
QY 121 EGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDTNTLYYWHRSLEKIHQCNIFREGQ 180
DB 121 EGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDTNTLYYWHRSLEKIHQCNIFREGQ 180
QY 181 YFGCSFDLTQVNDSSFEQHSQIMVKONAGIKPFSFNIVPLTSRVKPDPPHKNLSFHN 240
DB 181 YFGCSFDLTQVNDSSFEQHSQIMVKONAGIKPFSFNIVPLTSRVKPDPPHKNLSFHN 240
QY 241 DLYVQWENPQNFISRCCLFYEVVNNSTQTHNVFYVQAEKCNPEPERNVENTSCFMVPG 300
DB 241 DLYVQWENPQNFISRCCLFYEVVNNSTQTHNVFYVQAEKCNPEPERNVENTSCFMVPG 300
QY 301 VLPDPTLNTVRIRVKTNKLCEYDDKLSNWSQEMSIGKRNSTLYITMLLIVPVIAGAI 360
DB 301 VLPDPTLNTVRIRVKTNKLCEYDDKLSNWSQEMSIGKRNSTLYITMLLIVPVIAGAI 360
QY 361 VLLLYLKLRLKIIIFPPIDPGKIFKEMFGQNDQDTHLHWKYDIYEKQTEETDSVVLIN 420
DB 361 VLLLYLKLRLKIIIFPPIDPGKIFKEMFGQNDQDTHLHWKYDIYEKQTEETDSVVLIN 420
QY 421 LKASQ 426
DB 421 LKASQ 426
RESULT 2
AAW24973
ID AAW24973 standard; protein; 427 AA.
XX
AC AAW24973;
XX
DT 22-JUN-1998 (first entry)
XX

DE Human interleukin-13 alpha receptor.
XX Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13.
KW Homo sapiens.
OS WO9720926-A1.
PN 12-JUN-1997.
PD 07-NOV-1996; 96WO-FR001756.
PF 06-DEC-1995; 95FR-00014424.
PR (SNFI) SANOFI SA.
XX Caput D, Ferrara P, Laurent P, Vita N;
XX WPI; 1997-319773/29.
DR N-PSDB; AAT85827.
DR New purified human interleukin-13 receptors - and related nucleic acids,
XX useful for diagnosis and treatment of inflammation, allergy, etc.
PT Claim 8; Page 46-47; 83pp; French.
XX
CC This sequence represents interleukin-13 (IL-13) alpha receptor. The
CC invention relates to new purified peptides comprising 380 or 427 amino
CC acid sequences, which are receptors for interleukin-13 (IL-13); the 380
CC and 427 aa proteins are designated IL-13R beta and alpha respectively.
CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low
CC affinity, but acquires high affinity when associated with the IL-4
CC receptor. Nucleic acids encoding IL-13R beta and alpha are used as
CC diagnostic probes to identify aberrant synthesis or genetic anomalies
CC such as loss of heterozygosity and rearrangements, or chromosomal
CC anomalies. They are also used for production of recombinant IL-13R beta
CC and alpha which can be used as IL-13 antagonists, specifically to
CC regulate IL-13-induced responses for treatment of inflammation and
CC allergy. IL-13 receptors are also useful as antisense molecules for gene
CC therapy (blocking synthesis of IL-13R). Antibodies are used (in standard
CC immunoassays) to diagnose diseases associated with abnormal expression of
CC IL-13 receptors; when coupled to a toxin also for treatment of
CC overproduction of IL-13R. Cells that express IL-13R at the surface are
CC used to identify ligands and modulators of IL-13R
XX
SQ Sequence 427 AA;
Query Match 99.5%; Score 2309.5; DB 2; Length 427;
Best Local Similarity 99.8%; Pred. No. 4.4e-211;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MEWPARGLWALLLCAGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWNPPEGASSN 59
DB 1 MEWPARGLWALLLCAGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWNPPEGASSN 60
QY 60 NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLVGSGCSTNESEKPSILVEKICISP 119
DB 61 NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLVGSGCSTNESEKPSILVEKICISP 120
QY 120 PEGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDTNTLYYWHRSLEKIHQCNIFREG 179
DB 121 PEGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDTNTLYYWHRSLEKIHQCNIFREG 180
QY 180 QYFGCSFDLTQVNDSSFEQHSQIMVKONAGIKPFSFNIVPLTSRVKPDPPHKNLSFHN 239
DB 181 QYFGCSFDLTQVNDSSFEQHSQIMVKONAGIKPFSFNIVPLTSRVKPDPPHKNLSFHN 240
QY 240 DLYVQWENPQNFISRCCLFYEVVNNSTQTHNVFYVQAEKCNPEPERNVENTSCFMVPG 299
DB 241 DLYVQWENPQNFISRCCLFYEVVNNSTQTHNVFYVQAEKCNPEPERNVENTSCFMVPG 300
QY 300 GVLPTDPTLNTVRIRVKTNKLCEYDDKLSNWSQEMSIGKRNSTLYITMLLIVPVIAGAI 359
DB

Db 301 GVLPTLTNTVRIRVKTNKLCEYDDKLSNWSQEMSIGKRNSTLYITMLLIVPVIVAGAI 360
Qy 360 IVLLLYLRLKLIIFPPDPDGKIFKEMFGQNDTTLHWKKYDIYEKOTKEETDSVLLIE 419
Db 361 IVLLLYLRLKLIIFPPDPDGKIFKEMFGQNDTTLHWKKYDIYEKOTKEETDSVLLIE 420
Qy 420 NLKXASQ 426
Db 421 NLKXASQ 427

RESULT 3
AAB19807
ID AAB19807 standard; protein; 427 AA.
AC AAB19807;
XX DT 05-MAR-2001 (first entry)
XX Human interleukin-13 receptor alpha-1.
XX Interleukin-13 receptor alpha-1; interleukin-4; human; atopy;
KW atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;
KW dermatological; antiasthmatic; antiallergic; therapy; diagnosis.
XX OS Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..26
FT /label= Sig_peptide
FT Domain 27..347
FT /label= Extracellular_domain
FT Protein 28..427
FT /label= Mature_protein
FT Peptide 327..331
FT /note= "WSXWS motif conserved in the type-1 cytokine
FT receptor superfamily"
FT Domain 348..367
FT /label= Transmembrane_domain
FT Domain 368..427
FT /label= Cytoplasmic_domain
FT Binding-site 405..408
FT /note= "YXQ motif, consensus for STAT binding"
XX US6143871-A.
XX PN 07-NOV-2000.
XX PD 12-NOV-1997; 97US-00969125.
XX PF 13-DEC-1996; 96GB-00025899.
XX PR (GAUC/) GAUCHAT J.
XX PA (BONN/) BONNEFOY J.
XX PI Gauchat J, Bonnefoy J;
XX WPI; 2001-006445/01.
XX DR N-PSDB; AAA88907.
XX PT Novel polypeptide capable of binding interleukin-13 or interleukin-4
PT useful for treating atopy, atopic dermatitis, allergies, rhinitis,
PT eczema, asthma or AIDS.
XX Claim 2; Fig 1A; 26pp; English.
XX The present sequence is that of a protein capable of binding human
XX interleukin-13 (IL-13) and/or human interleukin-4 (IL-4) in the presence
XX of IL-4 receptor alpha. It was deduced from cDNA (see AAA88907) isolated
XX from a human activated tonsillar cDNA library. This IL-13 receptor alpha-1
XX polypeptide can be used to inhibit IL-13 or IL-4 induced Ige synthesis in
XX B cells, useful in the treatment of diseases in which Ige or Th2
XX differentiation plays a role, e.g. atopy, atopic dermatitis, allergy,

CC rhinitis, eczema, asthma or AIDS. Antibodies raised against the
CC polypeptide are useful for detecting IL-13 and IL-4 receptor or parts of
CC them which have been shed from cells as a result of disease, e.g. cancer,
CC leukaemia, atopy, atopic dermatitis, allergies, rhinitis, eczema, asthma,
CC lupus erythematosus, AIDS, thyroiditis, diabetes, uveitis, dermatitis,
CC psoriasis, urticaria, nephrotic syndrome, inflammatory bowel disease,
CC glomerulonephritis, ulcerative colitis, Crohn's disease, Sjogren's
XX syndrome and toxoplasmosis
SQ Sequence 427 AA;
Query Match 99.5%; Score 2309.5; DB 4; Length 427;
Best Local Similarity 99.8%; Pred. No. 4.4e-211;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 MEWPARLCGLWALLLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 59
Db 1 MEWPARLCGLWALLLCAGGGGGGAAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 60
Qy 60 NCSLWYFSHFQDKQDKKIAPETRSIEVPLNERICLQVGSQCSTNESEKPSILVEKICISP 119
Db 61 NCSLWYFSHFQDKQDKKIAPETRSIEVPLNERICLQVGSQCSTNESEKPSILVEKICISP 120
Qy 120 PEGDPESAATVTELOCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCNIFREG 179
Db 121 PEGDPESAATVTELOCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCNIFREG 180
Qy 180 QYFGCSFDLTVKVDSFEQHSVQIMVKDNAGIKPSFNIVPLTSRVKPPDPHINKLSFHN 239
Db 181 QYFGCSFDLTVKVDSFEQHSVQIMVKDNAGIKPSFNIVPLTSRVKPPDPHINKLSFHN 240
Qy 240 DDLYVQWENPQNFISRCILFYEVVNSQTEHNVFYVQEAECENPEFERNVENTSCFVWP 299
Db 241 DDLYVQWENPQNFISRCILFYEVVNSQTEHNVFYVQEAECENPEFERNVENTSCFVWP 300
Qy 300 GVLPTLTNTVRIRVKTNKLCEYDDKLSNWSQEMSIGKRNSTLYITMLLIVPVIVAGAI 359
Db 301 GVLPTLTNTVRIRVKTNKLCEYDDKLSNWSQEMSIGKRNSTLYITMLLIVPVIVAGAI 360
Qy 360 IVLLLYLRLKLIIFPPDPDGKIFKEMFGQNDTTLHWKKYDIYEKOTKEETDSVLLIE 419
Db 361 IVLLLYLRLKLIIFPPDPDGKIFKEMFGQNDTTLHWKKYDIYEKOTKEETDSVLLIE 420
Qy 420 NLKXASQ 426
Db 421 NLKXASQ 427
RESULT 4
ADL71812
ID ADL71812 standard; protein; 427 AA.
XX AC ADL71812;
XX DT 20-MAY-2004 (first entry)
XX Human interleukin-13 receptor alpha (IL-13 Ralpha) protein.
XX Human; IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis;
KW eczema; asthma; AIDS; gene therapy; interleukin; receptor.
XX OS Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..26
FT /label= Signal_peptide
FT Protein 27..427
FT /note= "Human mature IL-13 R protein"
FT Domain 27..347
FT /note = Extracellular domain
FT Domain 327..331
FT /note = WSXWS motif
FT Domain 368..427

FT	/note = Cytoplasmic domain	
XX		
PN	US2004043921-A1.	
XX	04-MAR-2004.	
XX	29-SEP-2003; 2003US-00671697.	
XX	13-DEC-1996; 96GB-00025899.	
PR	12-NOV-1997; 97US-00969125.	
PR	06-APR-2000; 2000US-00545002.	
XX	(BONN/) BONNEFOY J.	
PA	(GAUC/) GAUCHAT J.	
XX	Bonnefoy J, Gauchat J;	
XX	WPI; 2004-225726/21.	
DR	N-PSDB; ADL71811.	
XX	Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse	
PT	effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma	
PT	or AIDS, comprises administering a polypeptide or soluble polypeptide.	
XX	Claim 1; SEQ ID NO 9; 27pp; English.	
XX	The invention relates to polypeptides capable of binding human	
CC	interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpha. The	
CC	invention also relates to a method of treatment of a disease in which	
CC	IL13 and IL4 cause adverse effects. The method is useful for treating a	
CC	disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic	
CC	dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides	
CC	of the invention are useful in raising antibodies. It is also useful in	
CC	gene therapy. The present sequence is human interleukin-13 receptor alpha	
CC	(IL-13 Ralpha) protein.	
XX		
SQ	Sequence 427 AA;	
	Query Match	99.5%; Score 2309.5; DB 8; Length 427;
	Best Local Similarity	99.8%; Pred. No. 4.4e-211;
	Matches	426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY	1	MEWPARLCGLWALLLCAGGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 59
Db	1	MEWPARLCGLWALLLCAGGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 60
QY	60	NCSLWYFSHFQDKQDKKIAPETRRSIEVPLNERICLVQVSCSTNESEKPSILVEKICIS 119
Db	61	NCSLWYFSHFQDKQDKKIAPETRRSIEVPLNERICLVQVSCSTNESEKPSILVEKICIS 120
QY	120	PEGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDNTYTLYYWHSLEKIHQCENIFREG 179
Db	121	PEGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDNTYTLYYWHSLEKIHQCENIFREG 180
QY	180	QYFGCSFDLTNKKVDSFEQHSVOIMKDNAGKTKPSFNIVPLTSRVKPPPHIKNLSFNN 239
Db	181	QYFGCSFDLTNKKVDSFEQHSVOIMKDNAGKTKPSFNIVPLTSRVKPPPHIKNLSFNN 240
QY	240	DDLIVQWENPQNFISRCLFYEVEVNNSTQETHNVFVYQAEKCNPFERNVENTSCFMVP 299
Db	241	DDLIVQWENPQNFISRCLFYEVEVNNSTQETHNVFVYQAEKCNPFERNVENTSCFMVP 300
QY	300	GVLPDNLTVIRIVKTNKLCYEDDKLWSNWSQMSIGKKRNSTLYITMLLIVPVIIVAGAI 359
Db	301	GVLPDNLTVIRIVKTNKLCYEDDKLWSNWSQMSIGKKRNSTLYITMLLIVPVIIVAGAI 360
QY	360	IVLLLYLKRLLIIFPPIDPGKIFKEMFGDNDTLHWKKYDIYEKQTKETSDSVLLIE 419
Db	361	IVLLLYLKRLLIIFPPIDPGKIFKEMFGDNDTLHWKKYDIYEKQTKETSDSVLLIE 420
QY	420	NLKKASQ 426
Db	421	NLKKASQ 427

RESULT 5		
ADL82843		
ID	ADL82843 standard; protein; 427 AA.	
XX		
AC	ADL82843;	
XX		
DT	17-JUN-2004 (first entry)	
XX		
DE	Human PRO2537, SEQ ID 45.	
XX		
KW	Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;	
KW	Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;	
KW	Gene Therapy; PRO; B cell related disorder; cancer;	
KW	immune-mediated inflammatory disease; human.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2004024097-A2.	
XX		
PD	25-MAR-2004.	
XX		
PF	15-SEP-2003; 2003WO-US029097.	
XX		
PR	16-SEP-2002; 2002US-0411392P.	
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;	
PI	Wu TD;	
XX		
DR	WPI; 2004-329389/30.	
DR	N-PSDB; ADL82842.	
XX		
PT	New PRO polypeptide, useful for diagnosing and treating a B cell related	
PT	disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune	
PT	mediated hemolytic anemia, myaesthesia gravis or ankylosing spondylitis.	
XX		
PS	Claim 10; Fig 45; 695pp; English.	
XX		
CC	The present invention relates to PRO proteins and their coding sequences.	
CC	The PRO proteins are useful for diagnosing and treating a B cell related	
CC	disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide	
CC	antigen unresponsiveness, selective IgA deficiency, selective IgM	
CC	deficiency, selective deficiency of IgG subclasses, immunodeficiency with	
CC	hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's	
CC	lymphoma, intermediate lymphoma, follicular lymphoma, type II	
CC	hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic	
CC	anaemia, myaesthesia gravis, hypoadrenocorticism, glomerulonephritis, or	
CC	ankylosing spondylitis. The PRO proteins are also useful for preparing a	
CC	medicament for treating a condition that is responsive to the PRO	
CC	protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO	
CC	coding sequences are useful as hybridization probes in chromosome and	
CC	gene mapping, in preparing PRO proteins, or in generating transgenic	
CC	animals or knockout animals, which in turn are useful in the development	
CC	and screening of therapeutically useful reagents.	
XX		
SQ	Sequence 427 AA;	
	Query Match 99.5%; Score 2309.5; DB 8; Length 427;	
	Best Local Similarity 99.8%; Pred. No. 4.4e-211;	
	Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;	
QY	1	MEWPARLCGLWALLLCAGGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 59
Db	1	MEWPARLCGLWALLLCAGGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 60
QY	60	NCSLWYFSHFQDKQDKKIAPETRRSIEVPLNERICLVQVSCSTNESEKPSILVEKICIS 119
Db	61	NCSLWYFSHFQDKQDKKIAPETRRSIEVPLNERICLVQVSCSTNESEKPSILVEKICIS 120
QY	120	PEGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDNTYTLYYWHSLEKIHQCENIFREG 179

RESULT 5		
ADL82843	ADL82843 standard; protein; 427 AA.	
ID		
XX	ADL82843;	
AC		
XX	17-JUN-2004 (first entry)	
DT		
XX		
DE	Human PRO2537, SEQ ID 45.	
XX		
KW	Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;	
KW	Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;	
KW	Gene Therapy; PRO; B cell related disorder; cancer;	
KW	immune-mediated inflammatory disease; human.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2004024097-A2.	
XX		
PD	25-MAR-2004.	
XX		
PF	15-SEP-2003; 2003WO-US029097.	
XX		
PR	16-SEP-2002; 2002US-0411392P.	
XX	(GETH) GENENTECH INC.	
PA		
XX	Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;	
PI	Wu TD;	
PI		
XX	WPI; 2004-329389/30.	
DR	N-PSDB; ADL82842.	
XX		
PT	New PRO polypeptide, useful for diagnosing and treating a B cell related	
PT	disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune	
PT	mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.	
XX	Claim 10; Fig 45; 695pp; English.	
PS	The present invention relates to PRO proteins and their coding sequences.	
XX	The PRO proteins are useful for diagnosing and treating a B cell related	
CC	disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide	
CC	antigen unresponsiveness, selective IGA deficiency, selective IGM	
CC	deficiency, selective deficiency of IGB subclasses, immunodeficiency with	
CC	hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's	
CC	lymphoma, intermediate lymphoma, follicular lymphoma, type II	
CC	hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic	
CC	anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or	
CC	ankylosing spondylitis. The PRO proteins are also useful for preparing a	
CC	medicament for treating a condition that is responsive to the PRO	
CC	protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO	
CC	coding sequences are useful as hybridization probes in chromosome and	
CC	gene mapping, in preparing PRO proteins, or in generating transgenic	
CC	animals or knockout animals, which in turn are useful in the development	
CC	and screening of therapeutically useful reagents.	
XX		
XX	Sequence 427 AA;	
SQ		
Query Match 99.5%; Score 2309.5; DB 8; Length 427;		
Best Local Similarity 99.8%; Pred. No. 4.4e-211;		
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;		
QY	1	MEWPARLCGLWALLLCAGGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 59
Db	1	MEWPARLCGLWALLLCAGGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 60
QY	60	NCSLWYFSHFQDKDKIAPETRRSIEVPLNERICLVQVSCSTNESEKPSILVEKICIS 119
Db	61	NCSLWYFSHFQDKDKIAPETRRSIEVPLNERICLVQVSCSTNESEKPSILVEKICIS 120
QY	120	PEGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDNTYTLYYWHRSLEKIHQCENIFREG 179

Db	121	PEGDPESAVTELCQIWHNLSYMKCSWLPGRNTSPDNTYTYWHSLEKIHQCENIFREG	180	
Qy	180	OYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGIKPSFNIPLTSRVKPDPPHINKLSFHN	239	
Db	181	OYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGIKPSFNIPLTSRVKPDPPHINKLSFHN	240	
Qy	240	DDLXVQENPQNFISRCIFYEVEVNNQSTETHNVFYVQEAACENPEPERNVENTSCFMPV	299	
Db	241	DDLXVQENPQNFISRCIFYEVEVNNQSTETHNVFYVQEAACENPEPERNVENTSCFMPV	300	
Qy	300	GVLPDTLNTVIRVKTNKLCEYEDDKLWSNWSQEMSIGKRNSTLYITMLLIVPVIAGAI	359	
Db	301	GVLPDTLNTVIRVKTNKLCEYEDDKLWSNWSQEMSIGKRNSTLYITMLLIVPVIAGAI	360	
Qy	360	IVLLLYLRLKLIIFPPIDPGKIFKEMFGDQNDTTLHWKKYDIYEKQTEETDSVLLIE	419	
Db	361	IVLLLYLRLKLIIFPPIDPGKIFKEMFGDQNDTTLHWKKYDIYEKQTEETDSVLLIE	420	
Qy	420	NLKKASQ 426		
Db	421	NLKKASQ 427		
RESULT 6				
ID	ADN04504	standard; protein; 427 AA.		
XX	XX			
AC	ADN04504;			
DT	01-JUL-2004	(first entry)		
DE	Antipsoriatic protein sequence #445.			
KW	antipsoriatic; gene therapy; psoriasis; diagnosis.			
XX	XX			
OS	Homo sapiens.			
XX	XX			
PN	WO2004028479-A2.			
XX	XX			
PD	08-APR-2004.			
XX	XX			
PF	25-SEP-2003; 2003WO-US030907.			
XX	XX			
PR	25-SEP-2002; 2002US-0414006P.			
XX	XX			
PA	(GETH) GENENTECH INC.			
XX	XX			
PI	Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI, Wu TD;			
XX	XX			
DR	WPI; 2004-305105/28.			
DR	N-PSDB; ADN04503.			
XX	XX			
PT	New PRO nucleic acid or polypeptide, useful for preparing a			
PT	pharmaceutical composition for diagnosing or treating psoriasis in a			
PT	mammal.			
XX	XX			
PS	Claim 9; SEQ ID NO 898; 3069pp; English.			
XX	XX			
CC	The invention relates to novel polynucleotide and polypeptides for			
CC	treating psoriasis or a sequence having at least 80% identity to the			
CC	above sequences. The nucleic acid is useful for preparing a composition			
CC	for diagnosing or treating psoriasis in a mammal. This sequence			
CC	corresponds to one of the polypeptides of the invention.			
XX	XX			
SQ	Sequence 427 AA;			
Query Match				
Best Local Similarity 99.8%; Score 2309.5; DB 8; Length 427;				
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;				
Qy	1	MEWPARLGLWALLCAGGGGGGGG--APTETQPPVTNLSVSNLCTVIWTPNPEGASS	59	

Db	1	MEWPARGLGLWALLCAGGGGGGGGAAPTETQPPVTNLSVSNLCTVIWTPNPEGASS	60	
Qy	60	NCSLWYFSHFSGDKODKKIAPETRSEVPLNERICLOVGSQCSTNESEKPSILVEKICIS	119	
Db	61	NCSLWYFSHFSGDKODKKIAPETRSEVPLNERICLOVGSQCSTNESEKPSILVEKICIS	120	
Qy	120	PEGDPESAVTELCQIWHNLSYMKCSWLPGRNTSPDNTYTYWHSLEKIHQCENIFREG	179	
Db	121	PEGDPESAVTELCQIWHNLSYMKCSWLPGRNTSPDNTYTYWHSLEKIHQCENIFREG	180	
Qy	180	QYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGIKIPSFNIPLTSRVKPDPPHINKLSFHN	239	
Db	181	QYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGIKIPSFNIPLTSRVKPDPPHINKLSFHN	240	
Qy	240	DDLXVQENPQNFISRCIFYEVEVNNQSTETHNVFYVQEAACENPEPERNVENTSCFMPV	299	
Db	241	DDLXVQENPQNFISRCIFYEVEVNNQSTETHNVFYVQEAACENPEPERNVENTSCFMPV	300	
Qy	300	GVLPDTLNTVIRVKTNKLCEYEDDKLWSNWSQEMSIGKRNSTLYITMLLIVPVIAGAI	359	
Db	301	GVLPDTLNTVIRVKTNKLCEYEDDKLWSNWSQEMSIGKRNSTLYITMLLIVPVIAGAI	360	
Qy	360	IVLLLYLRLKLIIFPPIDPGKIFKEMFGQNDTTLHWKKYDIYEKQTEETDSVLLIE	419	
Db	361	IVLLLYLRLKLIIFPPIDPGKIFKEMFGQNDTTLHWKKYDIYEKQTEETDSVLLIE	420	
Qy	420	NLKKASQ 426		
Db	421	NLKKASQ 427		
RESULT 7				
ID	ADN62575	standard; protein; 427 AA.		
XX	XX			
AC	ADN62575;			
DT	12-AUG-2004	(first entry)		
DE	Human interleukin 13 (IL-13) receptor alpha 1 chain.			
XX	XX			
KW	Human; receptor; cytokine; interleukin 13 receptor alpha 1 chain; IL-13;			
KW	IL-4; atopy; atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;			
KW	cancer; inflammatory disease; rheumatoid arthritis;			
KW	inflammatory bowel disease; multiple sclerosis; Alzheimer's disease;			
KW	Lupus erythematosus; thyroiditis; diabetes; uveitis; psoriasis;			
KW	urticaria; nephrotic syndrome; glomerulonephritis; ulcerative colitis;			
KW	Crohn's disease; Sjogren's syndrome; toxoplasmosis; listeriosis; leprosy;			
KW	Lyme disease; tuberculosis; malaria; leishmaniasis.			
OS	Homo sapiens.			
XX	XX			
Key	Location/Qualifiers			
Peptide	1..26			
FT	/note= "Signal peptide"			
FT	27..427			
FT	/note= "Mature protein claimed in claim 1"			
XX	XX			
PN	US6743604-B1.			
XX	XX			
PD	01-JUN-2004.			
XX	XX			
PF	06-APR-2000; 2000US-00545002.			
XX	XX			
PR	13-DEC-1996; 96GB-00025899.			
PR	12-NOV-1997; 97US-00969125.			
XX	XX			
PA	(SMIK) SMITHKLINE BEECHAM CORP.			
XX	XX			
PI	Bonnefoy J, Gauchat J;			
XX	XX			
DR	WPI; 2004-409324/38.			

DR N-PSDB; ADN62574.
XX New isolated nucleic acid molecule encoding a polypeptide capable of
PT binding human IL-13 and/or binding human IL-4, useful in medicine, in
PT diagnostics or for producing antibodies.
XX
PT
XX
PS
XX
XX
CC The invention relates to an isolated nucleic acid molecule (ADN62574),
CC which encodes the mature form of a polypeptide capable of binding human
CC IL-13 (interleukin 13, a cytokine) and/or binding human IL-4 (designated
CC IL-13 receptor alpha 1 subunit) appearing as ADN62575. Also included are
CC a vector comprising the nucleic acid molecule and a host cell comprising
CC the vector. The nucleic acids are useful as probes or primers or in the
CC analysis of allelic variation. The polypeptides are useful for binding
CC human IL-13 and/or binding human IL-4 and act as inhibitors by
CC interfering with the interaction between human IL-13 or IL-4 and their
CC natural receptors. They can also be used in medicine, e.g. for treatment
CC of diseases such as atopy, atopic dermatitis, allergy, rhinitis, eczema,
CC asthma, AIDS, cancer, inflammatory disease (e.g. rheumatoid arthritis and
CC inflammatory bowel disease), multiple sclerosis, Alzheimer's disease,
CC lupus erythematosus, thyroiditis, diabetes, uveitis, psoriasis,
CC urticaria, nephrotic syndrome, glomerulonephritis, ulcerative colitis,
CC Crohn's disease, Sjogren's syndrome, toxoplasmosis, listeriosis, leprosy,
CC Lyme disease, tuberculosis, malaria and leishmaniasis. They can also be
CC used for producing antibodies, which can be used for diagnosing diseases.
CC The present sequence represents IL-13 receptor alpha 1 subunit.
XX
SQ Sequence 427 AA;

Query Match 99.5%; Score 2309.5; DB 8; Length 427;
Best Local Similarity 99.8%; Pred. No. 4.4e-211;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MEWPARGLWALLLCAGGGGGG-APTETQPPVTLNLSVSVENLCTVIWTPNPPGASS 59
DB 1 MEWPARGLWALLLCAGGGGGGAAPTETQPPVTLNLSVSVENLCTVIWTPNPPGASS 60
QY 60 NCSLWYFHFSGDKQDKKIAPETRSTIEVPLNERICLVQVSGQCSSTNESEKPSILVEKICIS 119
DB 61 NCSLWYFHFSGDKQDKKIAPETRSTIEVPLNERICLVQVSGQCSSTNESEKPSILVEKICIS 120
QY 120 PEGDPESAVTELQCIWHNLSYMKCSMLPGRNTSPDNTYLYWHRSLKIHQCEINFREG 179
DB 121 PEGDPESAVTELQCIWHNLSYMKCSMLPGRNTSPDNTYLYWHRSLKIHQCEINFREG 180
QY 180 QYFGCSFDLTQVDSFEQHSVQIMVKDNAGKIKPSFNIPLTSRVKPPPHIKNLSFHN 239
DB 181 QYFGCSFDLTQVDSFEQHSVQIMVKDNAGKIKPSFNIPLTSRVKPPPHIKNLSFHN 240
QY 240 DDLVYQWENPQNFISRLCLFVEVNVNSQTEHNVFVQEAACNPFERNVENTSCFVMP 299
DB 241 DDLVYQWENPQNFISRLCLFVEVNVNSQTEHNVFVQEAACNPFERNVENTSCFVMP 300
QY 300 GVLPLDTLNTVIRKTNKLCYEDDKLWSNWSQMSIGKKENSTLYITMLLIVPVIIVAGAI 359
DB 301 GVLPLDTLNTVIRKTNKLCYEDDKLWSNWSQMSIGKKENSTLYITMLLIVPVIIVAGAI 360
QY 360 IVLLLYLKRLLKIIFFPIPPDGKIFKEMFGDQNDTLHWKKYDIYEKQKEETDSVVLIE 419
DB 361 IVLLLYLKRLLKIIFFPIPPDGKIFKEMFGDQNDTLHWKKYDIYEKQKEETDSVVLIE 420
QY 420 NLKKAQ 426
DB 421 NLKKAQ 427
RESULT 8
ABM82441
ID ABM82441 standard; protein; 427 AA.
XX
AC ABM82441;
XX

DT 18-NOV-2004 (first entry)
XX
DE Tumour-associated antigenic target (TAT) polypeptide PRO2537, SEQ:6271.
XX
KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
XX gene therapy; cytostatic.
OS Homo sapiens.
XX
PN WO2004030615-A2.
XX
PD 15-APR-2004.
XX
XX 29-SEP-2003; 2003WO-US028547.
PF
XX 02-OCT-2002; 2002US-0414971P.
PR (GETH) GENENTECH INC.
XX
PA Wu TD, Zhang Z, Zhou Y;
XX
PI WPI; 2004-347921/32.
XX
DR N-PSDB; ACN41073.
XX
XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
PS Claim 12; SEQ ID NO 6271; 7273pp; English.
XX
XX The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention
XX
SQ Sequence 427 AA;
Query Match 99.5%; Score 2309.5; DB 8; Length 427;
Best Local Similarity 99.8%; Pred. No. 4.4e-211;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MEWPARGLWALLLCAGGGGGG-APTETQPPVTLNLSVSVENLCTVIWTPNPPGASS 59
DB 1 MEWPARGLWALLLCAGGGGGGAAPTETQPPVTLNLSVSVENLCTVIWTPNPPGASS 60
QY 60 NCSLWYFHFSGDKQDKKIAPETRSTIEVPLNERICLVQVSGQCSSTNESEKPSILVEKICIS 119
DB 61 NCSLWYFHFSGDKQDKKIAPETRSTIEVPLNERICLVQVSGQCSSTNESEKPSILVEKICIS 120
QY 120 PEGDPESAVTELQCIWHNLSYMKCSMLPGRNTSPDNTYLYWHRSLKIHQCEINFREG 179
DB 121 PEGDPESAVTELQCIWHNLSYMKCSMLPGRNTSPDNTYLYWHRSLKIHQCEINFREG 179
XX

Db 121 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDTNNTLYYHRSLEKIHQECENIPREG 180
Qy 180 QYFGCSFDLTQVQDSSFEQHSVQIMVKDNAGKIKPESNIVPLTSRVKPDPPHINKLSFHN 239
Db 181 QYFGCSFDLTQVQDSSFEQHSVQIMVKDNAGKIKPESNIVPLTSRVKPDPPHINKLSFHN 240
Qy 240 DDLYVQWENPQNFISRCIFYEVEVNNSTQTHNFFVYQEAACENPEPERNVENTSCFWVP 299
Db 241 DDLYVQWENPQNFISRCIFYEVEVNNSTQTHNFFVYQEAACENPEPERNVENTSCFWVP 300
Qy 300 GVLPTDLTNTVIRVKTNKLCEYEDDKLMSNWSQEMSIGKRNSTLYITMLLIVPVIVAGAI 359
Db 301 GVLPTDLTNTVIRVKTNKLCEYEDDKLMSNWSQEMSIGKRNSTLYITMLLIVPVIVAGAI 360
Qy 360 IVLLLYLRLKLIIFPPPIPDGKIFKEMFGQNDTTLHWKKYDIYEKQKETSVDVLLIE 419
Db 361 IVLLLYLRLKLIIFPPPIPDGKIFKEMFGQNDTTLHWKKYDIYEKQKETSVDVLLIE 420
Qy 420 NLKQASQ 426
Db 421 NLKQASQ 427

RESULT 9
ADL71813
ID ADL71813 standard; protein; 427 AA.
XX AC
XX ADL71813;
XX 20-MAY-2004 (first entry)
XX Human interleukin-13 receptor alpha (IL-13 Ralpa) mutant, T1301.
XX Human; IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis;
KW eczema; asthma; AIDS; gene therapy; interleukin; receptor; mutant;
KW mutein.
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 130
FT /note= "Wild-type Thr is substituted with Ile"
XX
XX US2004043921-A1.
XX
XX 04-MAR-2004.
XX
XX 29-SEP-2003; 2003US-00671697.
XX
XX 13-DEC-1996; 96GB-00025899.
PR 12-NOV-1997; 97US-00969125.
PR 06-APR-2000; 2000US-00545002.
XX
XX (BONN/) BONNEROY J.
PA (GAUC/) GAUCHAT J.
XX
XX Bonnefoy J, Gauchat J;
XX
XX WPI; 2004-225726/21.
XX
XX Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse
FT effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma
PT or AIDS, comprises administering a polypeptide or soluble polypeptide.
XX
XX Claim 14; Page; 27pp; English.
XX
XX The invention relates to polypeptides capable of binding human
CC interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpa. The
CC invention also relates to a method of treatment of a disease in which
CC IL13 and IL4 cause adverse effects. The method is useful for treating a
CC disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic
CC dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides

CC of the invention are useful in raising antibodies. It is also useful in
CC gene therapy. The present sequence is human interleukin-13 receptor alpha
CC (IL-13 Ralpa) mutant protein. Note: This sequence is not shown in the
CC specification, however it is constructed based on human IL-13 Ralpa
CC protein shown as SEQ ID NO:9 in the specification.
XX

SQ Sequence 427 AA;
Query Match 99.3%; Score 2303.5; DB 8; Length 427;
Best Local Similarity 99.5%; Pred. No. 1.7e-210;
Matches 425; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 1 MEMPARGCGLWALLLCAGGGGGG-APTETQPPVTNLSVSVENLCTVITWNPPEGASS 59
Db 1 MEMPARGCGLWALLLCAGGGGGGAAPTETQPPVTNLSVSVENLCTVITWNPPEGASS 60
Qy 60 NCSLWYFSHFGDKQDKKIAPIETRRSIEVPLNERICLOVGSQCSNNESEKPSILVEKCI 119
Db 61 NCSLWYFSHFGDKQDKKIAPIETRRSIEVPLNERICLOVGSQCSNNESEKPSILVEKCI 120
Qy 120 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDTNNTLYYHRSLEKIHQECENIPREG 179
Db 121 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDTNNTLYYHRSLEKIHQECENIPREG 180
Qy 180 QYFGCSFDLTQVQDSSFEQHSVQIMVKDNAGKIKPESNIVPLTSRVKPDPPHINKLSFHN 239
Db 181 QYFGCSFDLTQVQDSSFEQHSVQIMVKDNAGKIKPESNIVPLTSRVKPDPPHINKLSFHN 240
Qy 240 DDLYVQWENPQNFISRCIFYEVEVNNSTQTHNFFVYQEAACENPEPERNVENTSCFWVP 299
Db 241 DDLYVQWENPQNFISRCIFYEVEVNNSTQTHNFFVYQEAACENPEPERNVENTSCFWVP 300
Qy 300 GVLPTDLTNTVIRVKTNKLCEYEDDKLMSNWSQEMSIGKRNSTLYITMLLIVPVIVAGAI 359
Db 301 GVLPTDLTNTVIRVKTNKLCEYEDDKLMSNWSQEMSIGKRNSTLYITMLLIVPVIVAGAI 360
Qy 360 IVLLLYLRLKLIIFPPPIPDGKIFKEMFGQNDTTLHWKKYDIYEKQKETSVDVLLIE 419
Db 361 IVLLLYLRLKLIIFPPPIPDGKIFKEMFGQNDTTLHWKKYDIYEKQKETSVDVLLIE 420
Qy 420 NLKQASQ 426
Db 421 NLKQASQ 427

RESULT 10
ADL71835
ID ADF17835 standard; protein; 427 AA.
XX AC
XX ADF17835;
XX
XX 12-FEB-2004 (first entry)
XX
XX Human IL-13 alpha 1 receptor (IL-13R) protein.
KW IL-13R; human; receptor; anaphylaxis; hay fever; asthma;
KW antiinflammatory; cytostatic; antiulcer; dermatological; antiallergic;
KW antiasthmatic; fibrosis; Hodgkin's disease; ulcerative colitis;
KW scleroderma; allergic rhinitis; oncological;
KW chronic obstructive pulmonary disease.
XX Homo sapiens.
XX
XX WO2003080675-A2.
XX
XX 02-OCT-2003.
XX
XX 21-MAR-2003; 2003WO-AU000352.
XX
XX 22-MAR-2002; 2002AU-00001301.
PR 03-FEB-2003; 2003AU-00900437.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD. PA

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XX PI Dunlop FM, Baca M, Nash AD, Fabri LJ;
XX WPI; 2003-876912/81.
XX N-PSDB; ADF17834.
XX New monoclonal antibodies against interleukin-13 receptor alpha, useful
XX for treating fibrosis, Hodgkin's disease, ulcerative colitis,
XX scleroderma, allergic rhinitis, oncological conditions, asthma or an
XX inflammatory disorder.
XX Disclosure; SEQ ID NO 4; 99pp; English.
XX
XX This invention relates to a novel antibodies that function as interleukin
XX -13 receptor alpha-1 chain (IL-13R alpha-1) antagonists and can be used
XX for treating certain conditions induced by IL-13. Specifically, it refers
XX to antibodies that bind to IL-13R alpha-1 and inhibit or modulate IL-13
XX and IL-4 induced signalling. IL-13 is a mediator in the immunostimulatory
XX system, such that it is involved in the induction of IgE, IgG4 and T-
XX helper cells and accordingly is implicated in conditions from anaphylaxis
XX to hay fever and asthma. As such, the present invention describes these
XX novel antibodies as antiinflammatory, cytostatic, antiulcer,
XX dermatological, antiallergic and antiasthmatic. The methods and
XX compositions are useful for treating various disorders including
XX fibrosis, Hodgkin's disease, ulcerative colitis, scleroderma, allergic
XX rhinitis, oncological conditions and chronic obstructive pulmonary
XX disease. This polypeptide sequence is the human IL-13 alpha 1 receptor
XX protein of the invention.
XX
XX Sequence 427 AA;
XX
XX Query Match 99.2%; Score 2302.5; DB 7; Length 427;
XX Best Local Similarity 99.5%; Pred. No. 2.1e-210;
XX Matches 425; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
XX
XX QY 1 MWPRLCGIALLLCAGGGGGGG-APTPTPTPTNLVSVENLCTVIWTWNPPEGASS 59
XX DB 1 MWPRLCGIALLLCAGGGGGGG-APTPTPTPTNLVSVENLCTVIWTWNPPEGASS 60
XX
XX 60 NCSLWYFHFSGDKQDKKIAPIETRRSIEVPLNERICLVQSGQCSNTESEKPSILVEKICIS 119
XX DB 61 NCSLWYFHFSGDKQDKKIAPIETRRSIEVPLNERICLVQSGQCSNTESEKPSILVEKICIS 120
XX
XX 120 PEGDPESAVTELOCIVHNLNLSYMKCSWLPGRNTSPDNTYLYYHRSLEKIHQCEINIFREG 179
XX DB 121 PEGDPESAVTELOCIVHNLNLSYMKCSWLPGRNTSPDNTYLYYHRSLEKIHQCEINIFREG 180
XX
XX 180 QYFGCSFDLTFKVKDSSFEQHSVQIMVKDNAGKIKPSFNIPLTSRVKPDPPHKNLSFHN 239
XX DB 181 QYFGCSFDLTFKVKDSSFEQHSVQIMVKDNAGKIKPSFNIPLTSRVKPDPPHKNLSFHN 240
XX
XX 240 DDLYVQWENPQNTFISRCIFYEVEVNNSTQTHNVFVYQEAKECNPEPERNVENTSCPMVP 299
XX DB 241 DDLYVQWENPQNTFISRCIFYEVEVNNSTQTHNVFVYQEAKECNPEPERNVENTSCPMVP 300
XX
XX 300 GVLPDNTLVTRIRVKNLKYEDDDKLSNNSQEMSIGKKNSTLYITMLLIVPVIAGAI 359
XX DB 301 GVLPDNTLVTRIRVKNLKYEDDDKLSNNSQEMSIGKKNSTLYITMLLIVPVIAGAI 360
XX
XX 360 IVLLLYLKRLLKIIFFPPIPPGKIFKEMFGDQNDTLHWKKYDIYKQTKETDTSVLLIE 419
XX DB 361 IVLLLYLKRLLKIIFFPPIPPGKIFKEMFGDQNDTLHWKKYDIYKQTKETDTSVLLIE 420
XX
XX 420 NLKQASQ 426
XX DB 421 NLKQASQ 427
XX
XX
XX RESULT 11
XX ADL71814
XX ID ADL71814 standard; protein; 427 AA.
XX
XX AC ADL71814;
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QY 240 DDLYVQWENPQNFISRCFLFYEVVNNSTQTHNVFYQEAECENPEFERNVENTSCFMVP 299
DB 241 DDLYVQWENPQNFISRCFLFYEVVNNSTQTHNVFYQEAECENPEFERNVENTSCFMVP 300
QY 300 GVLPTLTNTVIRVKTNKLCEYEDDKLWSNWSQMSIGKKRNSTLYITMLLIYPVIVAGAI 359
DB 301 GVLPTLTNTVIRVKTNKLCEYEDDKLWSNWSQMSIGKKRNSTLYITMLLIYPVIVADAI 360
QY 360 IVLLLYLRLKLIIPPPIDPGKIFKEMFGDQNDTTLHWKKYDIYEKQTKETSDSVLLIE 419
DB 361 IVLLLYLRLKLIIPPPIDPGKIFKEMFGDQNDTTLHWKKYDIYEKQTKETSDSVLLIE 420
QY 420 NLKQASQ 426
DB 421 NLKQASQ 427

RESULT 12
AAB19808
ID AAB19808 standard; protein; 427 AA.
XX
AC AAB19808;
XX
DT 05-MAR-2001 (first entry)
XX
DE Human interleukin-13 receptor alpha-1 variant.
XX
KW Interleukin-13 receptor alpha-1; interleukin-4; human; atopy;
KW atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;
KW dermatological; antiasthmatic; antiallergic; therapy; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..26
FT Domain 27..347
FT /label= Sig_peptide
FT /label= Extracellular_domain
FT Protein 28..427
FT /label= Mature_protein
FT Misc-difference 130
FT /note= "Gly in "
FT Peptide 327..331
FT /note= "WSXHS motif conserved in the type-I cytokine
FT receptor superfamily"
FT Domain 348..367
FT /label= Transmembrane_domain
FT Domain 368..427
FT /label= Cytoplasmic_domain
FT Binding-site 405..408
FT /note= "YXXQ motif, consensus for STAT binding"
XX
XX US6143871-A.
XX
XX 07-NOV-2000.
XX
XX 12-NOV-1997; 97US-00969125.
XX
XX 13-DEC-1996; 96GB-00025899.
XX
XX (GAUC/) GAUCHAT J.
XX (BONN/) BONNEFOY J.
XX
XX Gauchat J, Bonnefoy J;
XX
XX WPI; 2001-006445/01.
XX
XX Novel polypeptide capable of binding interleukin-13 or interleukin-4
XX useful for treating atopy, atopic dermatitis, allergies, rhinitis,
XX eczema, asthma or AIDS.
XX
XX Claim 4; -: 26pp; English.
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CC The present sequence is that of a claimed isolated polypeptide which is
CC capable of binding human interleukin-13 (IL-13) and/or human interleukin-
CC 4 (IL-4) in the presence of IL-4 receptor alpha. It differs from a
CC sequence (see AAB19807) deduced from isolated cDNA by having residue 130
CC as Ile rather than Thr and residue 358 as Asp rather than Gly. This IL-13
CC receptor alpha-1 polypeptides can be used to inhibit IL-13 or IL-4
CC induced IgG synthesis in B cells, useful in the treatment of diseases in
CC which IgE or Th2 differentiation plays a role, e.g. atopy, atopic
CC dermatitis, allergy, rhinitis, eczema, asthma or AIDS. Antibodies raised
CC against the polypeptide are useful for detecting IL-13 and IL-4 receptor
CC or parts of them which have been shed from cells as a result of disease,
CC e.g. cancer, leukaemia, atopy, atopic dermatitis, allergies, rhinitis,
CC eczema, asthma, lupus erythematosus, AIDS, thyroiditis, diabetes,
CC uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome,
CC inflammatory bowel disease, glomerulonephritis, ulcerative colitis,
CC Crohn's disease, Sjogren's syndrome and toxoplasmosis. Note: The present
CC sequence is not shown in the specification but is derived from the IL-13
CC receptor alpha 1 sequence given in figure 1 (see AAB19807)
XX
SQ Sequence 427 AA;
```

```
Query Match 99.0%; Score 2296.5; DB 4; Length 427;
Best Local Similarity 99.3%; Pred. No. 7.7e-210;
Matches 424; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 MEWPARLCGLWALLICAGGGGGGGG-APTETQPPVTNLSVSNELCTVIWTWNPPEGASS 59
DB 1 MEWPARLCGLWALLICAGGGGGGGGAAPTETQPPVTNLSVSNELCTVIWTWNPPEGASS 60
QY 60 NCSLWYFSGDKQDKKIAPETRRSIEVPLNERICLVGSCSTNSESKEPSILVEKCIISP 119
DB 61 NCSLWYFSGDKQDKKIAPETRRSIEVPLNERICLVGSCSTNSESKEPSILVEKCIISP 120
QY 120 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDTNTLYYWHRSLEKIHOCENIFREG 179
DB 121 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDTNTLYYWHRSLEKIHOCENIFREG 180
QY 180 QYFGCSFDLTQKXDSFFQHSVQIMVKDNAGKIKFSFNIVPLTSRVKPPPHIKNLSFHN 239
DB 181 QYFGCSFDLTQKXDSFFQHSVQIMVKDNAGKIKFSFNIVPLTSRVKPPPHIKNLSFHN 240
QY 240 DDLYVQWENPQNFISRCFLFYEVVNNSTQTHNVFYQEAECENPEFERNVENTSCFMVP 299
DB 241 DDLYVQWENPQNFISRCFLFYEVVNNSTQTHNVFYQEAECENPEFERNVENTSCFMVP 300
QY 300 GVLPTLTNTVIRVKTNKLCEYEDDKLWSNWSQMSIGKKRNSTLYITMLLIYPVIVAGAI 359
DB 301 GVLPTLTNTVIRVKTNKLCEYEDDKLWSNWSQMSIGKKRNSTLYITMLLIYPVIVADAI 360
QY 360 IVLLLYLRLKLIIPPPIDPGKIFKEMFGDQNDTTLHWKKYDIYEKQTKETSDSVLLIE 419
DB 361 IVLLLYLRLKLIIPPPIDPGKIFKEMFGDQNDTTLHWKKYDIYEKQTKETSDSVLLIE 420
QY 420 NLKQASQ 426
DB 421 NLKQASQ 427
```

```
RESULT 13
ADX97531
ID ADX97531 standard; protein; 414 AA.
XX
XX AC ADX97531;
XX
XX 21-APR-2005 (first entry)
XX
XX Pancreatic cancer associated human protein, SEQ ID 79.
XX
XX pancreas tumor; cytostatic.
XX
XX OS Homo sapiens.
XX
XX EP1471075-A2.
```

```
XX PD 27-OCT-2004.
XX PF 31-MAR-2004; 2004EP-00090124.
XX PR 31-MAR-2003; 2003DE-01015834.
XX (HINZ/) HINZMANN B.
PA (ROSE/) ROSENTHAL A.
PA (PILA/) PILARSKY C.
PA (DAHL/) DAHL E.
PA (SPEC/) SPECHT T.
PA (LICH/) LICHTNER R.
XX
XX Rosenthal A, Pilarsky C, Dahl E, Specht T, Bruemmendorf T;
PI Lichtner R, Staub E, Roepcke S, Li X;
XX
XX WPI: 2004-768082/76.
DR N-PSDB; ADX97460.
XX
XX New nucleic acid differentially expressed in pancreatic tumor tissue, for
PT use as diagnostic agents and in screening for therapeutic agents.
XX
XX Claim 2; SEQ ID NO 79; 28pp; German.
XX
XX The invention relates to a novel human nucleic acid sequence of the
CC pancreas and its encoded protein. The invention further comprises:
CC proteins and peptides, preferably isolated, that contain a sequence
CC encoded by the novel nucleic acid; and methods for diagnosis and
CC treatment of pancreatic cancer, using a substance that inhibits or binds
CC to the protein or its DNA, including: an antisense oligonucleotide, short
CC interfering RNA or ribozyme directed against the pancreatic protein, an
CC organic molecule, particularly having a molecular weight below 5000,
CC especially 300, that binds to the pancreatic DNA, an aptamer or
CC (monoclonal) antibody, preferably human or humanized, that binds to the
CC pancreatic DNA, or an anti-idiotypic antibody raised against the
CC monoclonal antibody, any of which may be derivatized with a reporter
CC group, cytotoxic compound, immunostimulant and/or radioisotope. The novel
CC human pancreatic proteins and their encoding DNA have cytostatic
CC activity. The novel sequences are useful for inhibiting transcription
CC and/or expression of genes and proteins associated with pancreatic
CC cancer. This sequence represents one of the novel human pancreatic
CC proteins of the invention. Note: This sequence is not shown in the
CC specification, it has been electronically downloaded from a DVD-ROM
CC provided with this specification by the European Patent Office.
XX
XX SQ Sequence 414 AA;

Query Match 96.1%; Score 2230.5; DB 8; Length 414;
Best Local Similarity 99.8%; Pred. No. 1.5e-203;
Matches 413; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 14 LLCAGGGGGGGG-APTETQPPVTNLSVSNELCTVIWTWNPPEGASNCSLWYFSHFGDK 72
DB 1 LLCAGGGGGGGGAAPTETQPPVTNLSVSNELCTVIWTWNPPEGASNCSLWYFSHFGDK 60
QY 73 QDKKIAPETRRISEVPLNERICLQVGSQCSTNESEKPSILVEKICISPEGDPESAVTELQ 132
DB 61 QDKKIAPETRRISEVPLNERICLQVGSQCSTNESEKPSILVEKICISPEGDPESAVTELQ 120
QY 133 CIWHNLSYMKCSWLPGRNTSPDNTYTLTYWHRSLKIHQCENTFREGQYFGCSFDLTKVK 192
DB 121 CIWHNLSYMKCSWLPGRNTSPDNTYTLTYWHRSLKIHQCENTFREGQYFGCSFDLTKVK 180
QY 193 DSSFEQHSVQIMWKDNAGKIKPSFNI VPLTSRVKPDPPHKNLSFHNDDLYVQWENPQN 252
DB 181 DSSFEQHSVQIMWKDNAGKIKPSFNI VPLTSRVKPDPPHKNLSFHNDDLYVQWENPQN 240
QY 253 ISRCLFYEVENNSQTETHNVFYVQAEKCNPFERNVENTSCFMVPGVLPDNTLVIR 312
DB 241 ISRCLFYEVENNSQTETHNVFYVQAEKCNPFERNVENTSCFMVPGVLPDNTLVIR 300
QY 313 VTKNLCYEDDKLWSNWSQEMSGKGRNSTLYITMLLI VPIVAGAIIVLLLLKRLKII 372
```

```
Db 301 VTKNLCYEDDKLWSNWSQEMSGKGRNSTLYITMLLI VPIVAGAIIVLLLLKRLKII 360
QY 373 IFPPIDPGKIFKEMFGDQNDTLHWKKYDIYEKQTKETSDSVVLIENTLKASQ 426
DB 361 IFPPIDPGKIFKEMFGDQNDTLHWKKYDIYEKQTKETSDSVVLIENTLKASQ 414

RESULT 14
AAU69132
ID AAU69132 standard; protein; 405 AA.
XX
XX AAU69132;
AC
XX
XX 29-JAN-2002 (first entry)
DT
XX Canine interleukin 13 receptor PcaIL-13Ralpha1 405.
DE
XX
XX Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IL-13Ralpha2; immunoglobulin heavy chain; IGG Fc;
KW immunoglobulin light chain; lambda; immunosuppressive; gene therapy;
KW immune response.
XX
XX Canis familiaris.
OS
XX
XX WO200177332-A2.
FN
XX
XX 18-OCT-2001.
PD
XX
XX 09-APR-2001; 2001WO-US011498.
PF
XX
XX 07-APR-2000; 2000US-0195659P.
PR
XX 07-APR-2000; 2000US-0195874P.
PR
XX (HESK-) HESKA CORP.
PA
XX
XX McCall CA, Tang L;
PI
XX
XX WPI: 2001-657172/75.
DR N-PSDB; AAS59954, AAS59956.
DR
XX
XX Novel isolated canine protein, preferably canine immunoglobulin G protein
PT or canine interleukin-13 receptor protein useful for regulating immune
PT response of an animal and for developing regulatory compounds.
XX
XX Claim 18; Page 164-165; 221pp; English.
PS
XX
XX The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13) receptor
CC protein, the nucleic acids encoding them, antibodies raised against them,
CC fusion proteins between the IGG and IL-13R proteins and methods of
CC isolating regulators of them. The regulators are useful for regulating an
CC immune response in a canine. The proteins useful to develop regulatory
CC compounds including inhibitors and activators that, when administered to
CC a canine in an effective manner, are capable of protecting canine from
CC disease mediated by IL-13Ralpha or IL-13. The regulators are useful for
CC treating canine IGG (heavy and/or light chain) and/or canine IL-13R
CC mediated responses. The molecules of the invention are useful to regulate
CC the immune response of an animal (e.g. by gene therapy). The present
CC sequence represents a protein of the invention
XX
XX SQ Sequence 405 AA;

Query Match 80.9%; Score 1878; DB 4; Length 405;
Best Local Similarity 85.2%; Pred. No. 6.1e-170;
Matches 345; Conservative 24; Mismatches 36; Indels 0; Gaps 0;

QY 22 GCGGAPETQPPVTNLSVSNELCTVIWTWNPPEGASNCSLWYFSHFGDKQDKKIAPET 81
DB 1 GGVAAPTETQPPVTNLSVSNELCTVIWTWNPPEGASPNCTLRYFSHFDNKQDKKIAPET 60
QY 82 RRSIEVPLNERICLQVGSQCSTNESEKPSILVEKICISPEGDPESAVTELQCIWHNLSYM 141
```

Db 61 HRSKEVPLNERICLQVGSQSTNESDNPISILVEKCTPPPEGDPSAVTELQCVWHNLSYM 120
Qy 142 KCSWLPGRNTSPDTNTLYYHRSLEKIHQENIFREGQYFGCSFDLTKKVDSSEFQHSV 201
Db 121 KCTLWPGNTSPDTNTLYYHSSLGKTLQCEDIYREGQHGICSFALTNLKDSSFEQHSV 180
Qy 202 QIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDDIYVQWENPQNFISRLCFEV 261
Db 181 QIMVKDNARKLRPFNFIVPLTSHVKPDPPHILKRLFFQGNLYVQWKPNQNFYSRCLSQV 240
Qy 262 EVNNSQTEHNVFVYQEAECENPEFERNVENTSCFMVPGVLPDLTNTVIRVTKNKLCE 321
Db 241 EVNNSQTEHNDIFVYVEAKQNSPEEGNLEGTICFMVPGVLPDLTNTVIRVTKNKLCE 300
Qy 322 DDKLSNWSQMSIGKKNSTLYITMLIVPVIIVAGAIIVLLVYKRLKIIIFPPIDPG 381
Db 301 DDKLSNWSQMSIGKKNSTLYITMLIVPVIIVAGAIIVLLVYKRLKIIIFPPIDPG 360
Qy 382 KIFKEMFGDQNDTLHWKXYDIYEKQTEEDSDVVLLENLKASQ 426
Db 361 KIFKEMFGDQNDTLHWKXYDIYEKQTEEDSDVVLLENLKASQ 405

RESULT 15
AA92208
ID AA92208 standard; protein; 793 AA.
XX
AC AA92208;
XX
DT 01-AUG-2000 (first entry)
XX
DE IL-13/IL-4 dual trap, IL-13-R-alpha-1, IL-4-R-alpha-Fc fusion protein.
XX
KW IL-13/IL-4 dual trap; cytokine; antagonist; CNTF; receptor;
KW fusion protein; cytostatic; immunomodulator; osteopathic.
XX
OS Synthetic;
OS Homo sapiens.
XX
FH Key
FT Protein 1.343
FT /label= human IL-13-R-alpha-1
FT /note= "extraCellular domain"
FT Protein 254..564
FT /label= IL-4-R-alpha
FT /note= "extracellular domain"
FT Peptide 344..353
FT /label= linker
FT Peptide 565..566
FT /label= linker
FT Protein 567..793
FT /label= human_Fc
XX
PN WO200018932-A2.
XX
PD 06-APR-2000.
XX
PF 22-SEP-1999; 99WO-US022045.
XX
PR 25-SEP-1998; 98US-0101858P.
PR 19-MAY-1999; 99US-00313942.
XX
PA (REG-) REGENERON PHARM INC.
XX
PI Stahl N, Yancopoulos GD;
XX
DR WPI; 2000-293165/25.
DR N-PSDB; AAA09050.
XX
PT Isolated nucleic acid molecule for treating cytokine-related diseases or
PT disorders encodes a fusion polypeptide capable of binding a cytokine to
PT form a nonfunctional complex.

PS
XX
XX This sequence shows an IL-13/IL-4 single chain dual trap fusion protein,
CC designated IL-13-R-alpha-1, IL-4-R-alpha. The invention concerns
CC production of antagonists to any cytokine that utilizes an alpha
CC specificity determining component, which when combined with the cytokine,
CC binds to a first beta signal transducing component to form a non-
CC functional intermediate which then binds to a second beta signal
CC transducing component causing beta-receptor dimerization, the soluble
CC alpha specificity determining component of the receptor (sR-alpha) and
CC the extracellular domain of the first beta signal transducing component
CC of the cytokine receptor (beta-1) are combined to form heterodimers (sR-
CC alpha:beta-1) that act as antagonist to the cytokine by binding the
CC cytokine to form a non-functional complex. The receptor components are
CC shared by cytokines such as the CNTF (ciliary neurotrophic factor) family
CC of cytokines. The invention provides the basis for the development of IL-
CC 6 antagonists, as they show that if, in the presence of a ligand, a non-
CC functional intermediate complex, consisting of the ligand, its alpha
CC receptor and its beta-1 receptor component, can be formed, it will
CC effectively block the action of the ligand. Effective antagonists of IL-6
CC or CNTF consist of heterodimers of the extracellular domains of the alpha
CC specificity determining components of their receptors and the
CC extracellular domain of gpl30. The resultant heterodimers, function as
CC high-affinity traps, rendering the cytokine inaccessible to form a signal
CC transducing complex with the native membrane-bound forms of their
CC receptor. The nucleic acids and polypeptides are useful for treating
CC cytokine-related diseases or disorders such as osteoporosis and primary
CC and secondary effects of cancer including multiple myeloma or cachexia
XX
SQ Sequence 793 AA;
Query Match 80.8%; Score 1875.5; DB 3; Length 793;
Best Local Similarity 99.4%; Pred. No. 2.8e-169;
Matches 341; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 1 MWPRLCGLWALLLCAGGGGGGGG-APTETQPPVTNLSVSVENLCTVITWNPEGASS 59
Db 1 MWPRLCGLWALLLCAGGGGGGGG-APTETQPPVTNLSVSVENLCTVITWNPEGASS 60
Qy 60 NCSLWYFSHFCDKQDKIAPETRRSIEVPLNERICLQVGSQSTNESKPSILVKECISP 119
Db 61 NCSLWYFSHFCDKQDKIAPETRRSIEVPLNERICLQVGSQSTNESKPSILVKECISP 120
Qy 120 PEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNTLYYHRSLEKIHQENIFREG 179
Db 121 PEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNTLYYHRSLEKIHQENIFREG 180
Qy 180 QYFGCSFDLTQKQSSFEQHSVQIMVKDNAGIKPSFNIVPLTSRVKDDPPHINKLSFHN 239
Db 181 QYFGCSFDLTQKQSSFEQHSVQIMVKDNAGIKPSFNIVPLTSRVKDDPPHINKLSFHN 240
Qy 240 DDLYVQWENPQNFISRLCFYEVVNNSTETHNVFYQEAECENPEFERNVENTSCFMVP 299
Db 241 DDLYVQWENPQNFISRLCFYEVVNNSTETHNVFYQEAECENPEFERNVENTSCFMVP 300
Qy 300 GVLPDTLNTVIRVTKNKLCEYEDDKLWSNWSQMSIGKKNST 342
Db 301 GVLPDTLNTVIRVTKNKLCEYEDDKLWSNWSQMSIGKKNST 343
Search completed: February 8, 2006, 21:59:08
Job time : 134.105 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 21:59:28 ; Search time 25.2554 Seconds
(without alignments)
1622.950 Million cell updates/sec

Title: US-10-036-568A-4
Perfect score: 2320
Sequence: 1 MEWPARLCGLWALLCAGGG.....QTKETDSVLIENLKKASQ 426

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1653	71.2	426	2 JC7773	IL-13ralpha 1 prot
2	318	13.7	415	2 S12357	interleukin-5 rece
3	294.5	12.7	420	2 S21052	interleukin-5 rece
4	269.5	11.6	348	2 JC7907	common cytokine re
5	229	9.9	335	2 A0267	interleukin-5 rece
6	228	9.8	400	2 S06945	granulocyte-macrop
7	207	8.9	373	2 A55718	interleukin-2 rece
8	205.5	8.9	369	2 I49280	interleukin-2 rece
9	202	8.7	369	2 A42565	interleukin-2 rece
10	197.5	8.5	831	2 J01655	prolactin receptor
11	190	8.2	610	2 A34631	lactogen receptor
12	189	8.1	310	2 A29884	prolactin receptor
13	189	8.1	412	2 A41070	prolactin receptor
14	189	8.1	610	2 A36116	prolactin receptor
15	186	8.0	581	2 I45971	prolactin receptor
16	185	8.0	616	2 A30304	prolactin receptor
17	183	7.9	292	2 I77525	prolactin receptor
18	180	7.8	303	2 I77524	prolactin receptor
19	180	7.8	608	2 I53269	prolactin receptor
20	176	7.6	630	2 I51086	prolactin receptor
21	173	7.5	918	2 A36337	membrane glycoprot
22	172.5	7.4	288	2 B59405	prolactin receptor
23	172.5	7.4	376	2 A59405	prolactin receptor
24	172.5	7.4	622	2 A40144	cytokine receptor
25	170	7.3	897	1 A39255	interleukin-3 rece
26	165	7.1	396	2 I52909	prolactin receptor
27	163	7.0	830	2 I50455	prolactin receptor
28	162.5	7.0	333	2 S13684	granulocyte-macrop
29	161.5	7.0	1092	2 JX0312	differentiation-st

30	157	6.8	378	2 A40266	interleukin-3 rece
31	157	6.8	896	1 A35782	cytokine receptor
32	156.5	6.7	378	2 S50040	granulocyte-macrop
33	154.5	6.7	896	2 I56563	interleukin-3 rece
34	149	6.4	878	1 A40091	interleukin-3 rece
35	146.5	6.3	608	2 S32823	somatotropin recep
36	145	6.2	638	2 A33991	somatotropin recep
37	144.5	6.2	1097	2 S17308	leukemia inhibitor
38	144	6.2	918	2 A44257	interleukin-6 sign
39	142.5	6.1	917	2 I49699	glycoprotein 130 -
40	141	6.1	638	2 S12136	somatotropin recep
41	140	6.0	638	2 E28176	somatotropin recep
42	139	6.0	508	1 ZUHUR	erythropoietin rec
43	139	6.0	634	2 S33339	somatotropin recep
44	135.5	5.8	286	2 S50039	granulocyte-macrop
45	134.5	5.8	557	2 A32694	interferon alpha/b

ALIGNMENTS

RESULT 1

JC7773
IL-13ralpha 1 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: JC7773
R:Pierrrot, C.; Beniguel, L.; Begue, A.; Khalife, J.
Biochem. Biophys. Res. Commun. 287, 969-976, 2001
A:Title: Expression of a functional IL-13ralpha by rat B cells.
A:Reference number: JC7773; PMID:11573960
A:Accession: JC7773
A:Molecule type: mRNA
A:Residues: 1-426 <PIE>
A:Cross-references: UNIPROT:Q8VHC2; UNIPARC:UPI000017CC49; GB:AY044251
C:Comment: This protein is an functionally binding protein involved in B cell proliferat
C:Genetics:
A:Gene: il-13ralpha

Query Match 71.2%; Score 1653; DB 2; Length 426;
Best Local Similarity 73.3%; Pred. No. 3e-121;
Matches 313; Conservative 43; Mismatches 67; Indels 4; Gaps 3;

Qy	1	MEWPARLCGLWALLCAGGGGGGAGTETPTPTNLSVSVENLCTVITWNPPEGASNN	60
Db	1	MARPAWLGELLVLLFAASLDQVALA-TEVOPPTNLSVSVENLCTVITWNPPEGASPN	59
Qy	61	CSLWYFSGHFGDKQDKIAPETRRSIEVPLNERICLVGSGCSTNESEKPSILVEKICISPP	120
Db	60	CSLAYFSHFDQDKKIAPETRRKKELPLNEKICLVGSGCSTNESEKPSPLVKKICISPP	119
Qy	121	EGDPESAVTELOCTWHNLSYMKCSWLPGRNTSPDNTYLYWHRSLEKIHOCENIFREQQ	180
Db	120	RGSESATVTELOCTWHNLSYMKCSWLPGRNTSPDNTYLYWYSSLGSKSQENIHREQQ	179
Qy	181	YFGCSFDLTVKDSSFEOHSVQIMVKONAGIKPSFNIVPLTSRVKPPPHIKNLSFHND	240
Db	180	HIGCSFKLTKV-ESNYEHNQIMVKONAGIKRPSYKIVSFTSNVKGPPPHIKHLFKNG	238
Qy	241	DLTYQWENPQNFISCLFYEVVNNSTQETH--NVFYVOEAKCENPERNVNVENTSCFMV	298
Db	239	ALFVQWKPNQFSSRCLSYEVVNSTQTSYNSNSLEVEEDKCNSEFDRNMEGASCFIS	298
Qy	299	PGVLDPDTLVTRIRVKTNKLCTYEDDKLNSWQESIGKKRNTLYITMLLVPVIVAGA	358
Db	299	PGVLNTVTVTRVKTNKLCTFDDNDLNSWSEALSIGKPNSTFTYTMLLIIPVAVV	358
Qy	359	ITVLLYLKRLKIIIFPPIPDGKIFKMFQDNDTLHWKKYDIYEKQKETSDSVLI	418
Db	359	IIILLFYLRKLIIFPPIPDGKIFKMFQDNDTLHWKKYDIYEKQKETSDSVLI	418
Qy	419	ENLKKAS 425	

Db 419 ENLKAA 425

RESULT 2
S12357
interleukin-5 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S12357
R:Takaki, S.; Tominaga, A.; Hitoshi, Y.; Mita, S.; Sonoda, E.; Yamaguchi, N.; Takatsu, K.
EMBO J. 9, 4367-4374, 1990
A:Title: Molecular cloning and expression of the murine interleukin-5 receptor.
A:Reference number: S12357; MUID:91092260; PMID:2265612
A:Accession: S12357
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-415 <TAK>
A:Cross-references: UNIPROT:P21183; UNIPARC:UPI0000028472; GB:D90205; NID:g220465; PIDN:
C:Keywords: cytokine receptor; transmembrane protein

Query Match 13.7%; Score 318; DB 2; Length 415;
Best Local Similarity 23.9%; Pred. No. 4.2e-17;
Matches 97; Conservative 74; Mismatches 179; Indels 56; Gaps 14;

QY 32 PPVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWYFSHF-GDKQDKKIAPETRERSIEVPL 89
Db 29 PPV-NFTIKATGLAQVLLHWDPNPQEQRRHVDLEYHVKNAPQEDBYDTRKTESKCVTEPL 87

QY 90 NERICLQVGSQSTNESEKPSILVERKICISPPGEGDPESAIVTELCQIWHNL----- 138
Db 88 HEGFAASVTRILKSSHTTLASSWVSAELKAPGSPGTSVNLCTCTHTTVVSSHILRPYQ 147

QY 139 SYMKCSWLPGRNTPPTNTLYIYWHRSLEKIHQCNIFRE--GQYFGCSFDLTQVKDSSP 196
Db 148 VSLRCTWLVGKADPEDTQYFLYRFGVLTE--KCQESYRDALNRNACWFRPTFINSKGF 205

QY 197 EQHSVQIMVKONAGKIKPSFNIVPLTSRVKPPDPHKNLSFHNDDLYVQWENPQN-FISR 255
Db 206 EQLVHNGSSKRAAIKPFQDPSLAIDQVNPFRNVTQVIESNLSYIQWEXPLSAFDPH 265

QY 256 CLFYEVEVNSQPTETHNFVYQBAKCNPEFERNVENTSCFMVPGVPLDTLNTVRIRVKT 315
Db 266 CFNYELKIYTRNG-----HIQKEKLIANKFISKIDDVSTY-----SIQVRAV 309

QY 316 NKLCEYEDDKLWNSWQEMSIGKRNSTLYITMLLIVPVIVAGAIIVLLYLKRLKII----- 372
Db 310 SSPCRMFGPR-WGEWSQPIYVGERKS-LVEWHILVLP--TAACFVLLIFSLICRVCHLW 364

QY 373 --IFPPDPGKIFKEMFGQNDTTLHWKKYDIYEKQTEEDSVV 416
Db 365 TRLFPVPAPKSNIKDL-----PVTVEYKPSNETKIEVV 399

RESULT 3
S21052
interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored is
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S21052; S21050; S21053; A46175; S78106; S78107
R:Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tominaga, A.; Takatsu, K.
J. Exp. Med. 175, 341-351, 1992
A:Title: Molecular cloning and expression of the human interleukin 5 receptor.
A:Reference number: S21050; MUID:92121815; PMID:1732409
A:Accession: S21052
A:Molecule type: DNA
A:Residues: 1-420 <MUR>
A:Cross-references: UNIPROT:Q14633; UNIPARC:UPI00000729BE; EMBL:X61176; NID:g33843; PIDN:
A:Experimental source: clone lambda h5R.12
A:Accession: S21050
A:Molecule type: DNA
A:Residues: 1-395,'I', <MU2>
A:Cross-references: UNIPARC:UPI0000179A7F; EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID
A:Experimental source: clone lambda h5R.27

A:Accession: S21053
A:Molecule type: mRNA
A:Residues: 1-332,'K', <MU3>
A:Cross-references: UNIPARC:UPI0000179A80; EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID
A:Experimental source: clone lambda h5R.25
R:Tavernier, J.; Tuytens, T.; Plaetinck, G.; Verhee, A.; Fiers, W.; Devos, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 7041-7045, 1992
A:Title: Molecular basis of the membrane-anchored and two soluble isoforms of the human
A:Reference number: A46175; MUID:92357767; PMID:1495999
A:Accession: A46175
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 333-420 <TAV>
A:Cross-references: UNIPARC:UPI0000179A81
A:Experimental source: HL-60 cells and eosinophils
A>Note: sequence extracted from NCBI backbone (NCBIN:116243, NCBIP:116244)
R:Murata, Y.
submitted to the EMBL Data Library, July 1991
A:Reference number: S78106
A:Accession: S78106
A:Molecule type: DNA
A:Residues: 1-128,'I',130-395,'I', <MUW>
A:Cross-references: UNIPARC:UPI000006EDIC; EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID
R:Murata, Y.
submitted to the EMBL Data Library, September 1991
A:Reference number: S78107
A:Accession: S78107
A:Molecule type: mRNA
A:Residues: 1-128,'I',130-332,'K', <MU4>
A:Cross-references: UNIPARC:UPI00006D11E; EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID
C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-420/Product: interleukin-5 receptor alpha chain #status predicted <MAT>
F;345-365/Domain: transmembrane #status predicted <TM>
F;35,131,137,142,216,244/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.7%; Score 294.5; DB 2; Length 420;
Best Local Similarity 24.8%; Pred. No. 2.9e-15;
Matches 102; Conservative 65; Mismatches 180; Indels 65; Gaps 16;

QY 32 PPVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWYFSHFQDKQDKKIAPETRERSIEVPLN 90
Db 32 PPV-NFTIKVTGLAQVLLQWKPNPDQEQRNLEY-----QVKINAPK-EDDYETRIT 82

QY 91 ERICLQV-----GSQCSTNESEKPSILVEKCTIS-----PPEGDPESAIVTELCQIWHNL--- 138
Db 83 ESKCVTILHKGFSASVRTILQNDHSLSSASAEHLHAPPSPGTSVNLCTCTTTTTEDN 142

QY 139 -----SY---MKCSWLPGRNTPPTNTLYIYWHRSLEKIHQCNIFRE--GQYFGCSFDL 188
Db 143 YSRLRSYQVSLHCTWLVGTDAPEDTQYFLYIRYGSWTE--ECQEYSKDTLGRNIACWFP 200

QY 189 TKVQDSSFPQHSVQIMVKONAGKIKPSFNIVPLTSRVKPPDPHKNLSFHNDDLYVQWEN 248
Db 201 TILSKGRDMLAVLVNNGSSKHSARIPFDQLFALHAIDQINPLNVTAEIEGTLSIQWEK 260

QY 249 PQN-FISRCLFYEVEVNSQPTETHNFVYQBAKCNPEFERNVENTSCFMVPGVPLDTLN 307
Db 261 PVSAPFIHCFDEYVKIHNRNG-----YLQIEKLMTNAFISIIDLISKY----- 304

QY 308 TVRIRVKTNKLCEYEDDKLWNSWQEMSIGKRNSTLYITMLLIVPVIVAGAIIVLLYLK 367
Db 305 DVQVRAAVSSMCREAG-LWSEWSQPIYVGNDEHKPLREWFVIVIMATIFILLILSLICK 363

QY 368 --RLKIIIPPIPDGKIFKEMFGQNDTTLHWKKYDIYEKQTEEDSVV 417
Db 364 ICHLWIKLFPPIAPKSNIKDLFVITN-----YEKAGSSETEIEVI 404

RESULT 4
JC7907
common cytokine receptor gamma chain, isoform a - chicken
C:Species: Gallus gallus (chicken)

C;Accession: JC7907
E;Min, W.: Lillehoj, H.S.; Fetterer, R.H.
Biochem. Biophys. Res. Commun. 299, 321-327, 2002
A;Title: Identification of an alternatively spliced isoform of the common cytokine receptor
A;Reference number: JC7907; MUID:2325486; PMID:12437989
A;Accession: JC7907
A;Molecule type: mRNA
A;Residues: 1-348 <MIN>
A;Cross-references: UNIPROT:Q8AUP2; UNIPARC:UPI00000PB604; GB:AJ419897; GB:AJ419898
A;Experimental source: e99
C;Comment: This protein, expressed as a transmembrane glycoprotein, is a novel member of
ment and proliferation.
C;Genetics:
A;Gene: ch gamma-c-a

		Best Local Similarity	26.2%; Pred. No. 2e-13;	Matches	85; Conservative	60; Mismatches	125; Indels	55; Gaps	15;
Qy	118	SP-PEGDPESAVTBLOCIWNNLSYMKCSWIJPGRWNTSPDWTLYLWHRSLKHIQCEN-I	175	:	:	:	:	:	:
Dd	23	SPSPKG-----VECILFNEEYMTCTGSGQTLT--ANYSLYYIYENKLPPVCECOYL	72	:	:	:	:	:	:
Qy	176	PREGQYFGCSPDLTKVDSDSFHQHSQIMVKDNAGIKPSEINIVPLTSRVKPPDPPIHKNL	235	:	:	:	:	:	:
Dd	73	WDRSVRIGCRPEQSEI--IQQAFYFVNASCNQGOTLEIPSNRMELQNLYKKPEAP--VNL	128	:	:	:	:	:	:
Qy	236	SFHN---DDLTVQVENQNFISRCGLFYEEV-VNNSQTETHNVFVQAKCENPEFRNVE	291	:	:	:	:	:	:
Dd	129	TIHMSGNQQLQTWSSPY-PKEOCLHEHVKYKSNKDTSWTN-----QEVK-----	172	:	:	:	:	:	:
Qy	292	NWSCFWPGVLPTLINTVRIKVTNKLCEYDDKLWNWSQEMSIGCKRNST-----	342	:	:	:	:	:	:
Dd	173	-GVIFPSPVUDYEKYFFYFVASKINNVC-GNTQLMSESVVPFWG--NNSTSKGVAEEQL	228	:	:	:	:	:	:
Qy	343	----LYITMLIIVPVI VAGAIIVLLLVLRUKLIIFPPIDPDGKI FKEMFGDQNDTLHW	398	:	:	:	:	:	:
b	229	OWFMHTVGIPIASCLALLVLAVLLVMRRVWVLIIMPRI NPNPSKNFDOLFTHNGDFQEW	288	:	:	:	:	:	:

A40267
interleukin-5 receptor alpha chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 09-Jul-2004
C:Accession: A40267
R:Tavernier, J.; Devos, R.; Cornelis, S.; Tulpens, T.; Van der Heyden, J.; Fiers, W.; Pl
Cell 66, 1175-1184, 1991
A:Title: A human high affinity interleukin-5 receptor (IL5R) is composed of an IL5-speci
A:Reference number: A40267; MUID:92005669; PMID:1833065
A:Accession: A40267
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-335 <TAV>
A:Cross-references: UNIPROT:001344; UNIPARC:UPI000002ABD4; GB:M75914; NID:g186387; PIDN
C:Keywords: cytokine receptor; transmembrane protein

[illegible]

Qy	139	-----SY-----MKCSWLPGRNTSPDNTNTLYWHRSLKIHOCENIFRE--QYFGCSPLD	180
Db	143	YSLRYSQVSLHCTWLVTGTDAPEDTQFLYRYRGSWTB--ECQEYSKOTLGRNIACWFFR	200
Qy	189	TKWKDSFEQHSQVIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIQNLSFHNDLLVYQVEN	248
Db	201	TFILSKGRDWSLVANGSSKHSARPPDQLFALHAIDQINPLNVTABIEGTRLSIQWEK	260
Qy	249	PQN-FISRCLFYREVEVNSQTETHNVFYQVEAKCENPERFNVNTSCFMVGPVLPDTLN	307
Db	261	PVSAPPIHCFDEYVEKIHNTRNG-----YLQIEKLMTNAFISIIDLSKY-----	304
Qy	308	TVTRVRVTKNLCEYDDDKLWSNWSQEMSIGKIKR	339
Db	305	DVQVRAAVSSMCREAG-LMSEWSQPIYVGFSR	335

S06945
granulocyte-macrophage colony-stimulating factor receptor A precursor - human
NAlternate names: GM-CSF receptor alpha chain; hemopoietic growth factor receptor
C/Species: Homo sapiens (man)
C/Date: 22-Jan-1993 #sequence.revision 22-Jan-1993 #text_change 09-Jul-2004
C/Accession: S06945; A1286; A4474
R/Gearing, D.P.; King, J.A.; Gough, N.M.; Nicola, N.A.
EMBO J. 8, 3667-3676, 1989
A>Title: Expression cloning of a receptor for human granulocyte-macrophage colony-stimulating factor
A/Reference number: S06944; MUID:90059966; PMID:2555171
A/Accession: S06945
A/Molecule type: mRNA
A/Residues: 1-400 <GEA>
A/Cross-references: UNIPROT:P15509; UNIPARC:UIP000000045; EMBL:X17648; NID:G32087; PIDN:
R:Croster, K.E.; Wong, G.G.; Matthey-Prevot, B.; Nathau, D.G.; Steff, C.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 7744-7748, 1991
A>Title: A functional isoform of the human granulocyte/macrophage colony-stimulating factor
A/Reference number: A1286; MUID:91352066; PMID:1715577
A/Accession: A1286
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 347-400 <CRO>
A/Cross-references: UNIPARC:UIP000017C141
R/Rappold, G.; Willson, T.A.; Henke, A.; Gough, N.M.
Genomics 14, 455-461, 1992
A>Title: Arrangement and localization of the human GM-CSF receptor alpha chain gene CSF2
A/Reference number: A4474; MUID:93052350; PMID:1358805
A/Accession: A4474
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 'M', 377-400 <RAP>
A/Cross-references: UNIPARC:UIP00000723FC; GB:A45539; NID:G258858; PIDN:AAB23942.1; PID
A/Note: sequence extracted from NCBI backbone (NCBIP:117980)
C/Genetics:
A/Gene: GDB:CSF2RA; CSF2R
A/Cross-references: GDB:118777; OMIM:306250; OMIM:425000
A/Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
C/Keywords: glycoprotein; growth factor receptor; transmembrane protein
P:1-22/Domain: signal sequence #status predicted <SIG>
P:23-400/Product: granulocyte-macrophage colony-stimulating factor receptor #status pre
P:232-346/Domain: transmembrane #status predicted <TM>
F:342-54, 99, 123, 135, 182, 195, 223, 229, 272, 305/Binding site: carbohydrate (Asn) (covalent)

[illegible]

QY 149 RNTSPDNTYLYYHRSLEKIHOCENIFRE-GQYFGCSFD-LTKVKDSSFEQHSVQIMVX 206
Db 142 PTAPRDVOYFLYIRNSKRREIRCPYIQDSGTHVGCHLNDLSGLTSRNT-----PLVN 195
QY 207 DNAGKIKPSF--NIVPLTSRVKPDPPHKKLSFHNDDLYYQWENPNQF--ISRCLF-YEV 261
Db 196 GTSREIGIQPDSLLDTFKIERFNPNSVTVRCNTTCLVWKQPPRYQKLSYLDFOYQL 255
QY 262 EVN--NSQTETHNVFYVOEAKCENPEFERNVENTSCFMVPGVLPTDLTNTVRIIRVKTNKL 319
Db 256 DVHRKNTQPGTENLLINVSGDLENR-----YNFSPSEPRAKHSVKIRAADVRL 304
QY 320 YEDDKLSNWSQEMSIGKKNS--TLYITMLLIVPVIVAGAIIVLLLYLRLKI-IIFPP 376
Db 305 N-----WSSSEAEFGSDGNLGSVYIYLLVGTGLVCG-IVLGFPLKRFRLRIORLFP 358
QY 377 IPDPGKIFKEMFGDON--DDTLHWKXYDIYE-KQTKEETDSV 415
Db 359 VPQ-----IKKLDNHNHEVEBIIWEFTPEGKGYYREELTV 396
RESULT 7
A55718
Interleukin-2 receptor gamma chain precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: A55718
R;Henthorn, P.S.; Somberg, R.L.; Fimiani, V.M.; Puck, J.M.; Patterson, D.P.; Felsburg, R.
Genomic 23, 69-74, 1994
A;Title: IL-2Rgamma gene microdeletion demonstrates that canine X-linked severe combined
A;Reference number: A55718; MUID:95130114; PMID:7829104
A;Accession: A55718
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-373 <HEN>
A;Cross-references: UNIPROT:P40321; UNIPARC:UPI00000128C41; GB:U04361; NID:9517411; PIDN:
C;Superfamily: interleukin-2 receptor gamma chain
C;Keywords: cytokine receptor; duplication
Query Match 8.9%; Score 207; DB 2; Length 373;
Best Local Similarity 25.1%; Pred. No. 1.7e-08;
Matches 76; Conservative 52; Mismatches 131; Indels 44; Gaps 14;
QY 87 VPLNERICLVGSGCSNNESEKLSILVEKICSPGDPESAATVTELOCIWNLSYMKCSWL 146
Db 21 VGLNSTVPMENG-----NEDITDPFLTATPSETLSVSLPLPEVQCFVFNVEYMNCTWN 75
QY 147 PGRNTSPDNTYLYYHRSLE--EKIHOCEN-IFREGQYFCGSFDLTKVKDSSFEQHSVQI 203
Db 76 SSSEPRP-TNLTLHYWYKNSNDKQVQCGHYLFSREVTAGCW--LQKEETHLYETTFVQL 132
QY 204 MVKDNAGKIKPSFNIVPLTSRVKPDPPHKKLSFHN--DDLXVWENPNQFISRCLFYE 260
Db 133 --RDPREPRQSQTKLQNLVLPWAP--ENLTLNLSQSLSWSN--RHLDHCLHVV 186
QY 261 VEYVNSQTETHNVFYVOEAKCENPEFERNVENTSCFMVPGVLPTDLTNTVRIIRVKTNKL 320
Db 187 VOYRSDWRDWT-----EQSVDRHNSFLSPSDVQCFYFTRVRSRYNPCLG 232
QY 321 EDDKLSNWSQEMSIGK--KRNSTLYITMLLIVPVIVAGAIIVLL---LYLKKLKIIFP 375
Db 233 SAQR--WSEWHPHWSGNTSKENPLFASEAVLIPGLSGMGLIISLCVYWLER-----SIP 287
QY 376 PIP 378
Db 288 RIP 290
RESULT 8
I49280
Interleukin-2 receptor gamma chain precursor - mouse
C;Species: Mus musculus (house mouse)

C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: I49280; A47514; JN0592; JN0775; S37582; I53398
R;Cao, X.; Kozak, C.A.; Liu, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993
A;Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R) gan
A;Reference number: A47514; MUID:93391374; PMID:8378320
A;Accession: I49280
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-369 <CAO>
A;Cross-references: UNIPROT:P34902; UNIPARC:UPI0000001949; EMBL:U21795; NID:G727349; PIDN:
A;Accession: A47514
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-369 <RE42>
A;Cross-references: UNIPARC:UPI0000001949; GB:I20048; NID:G404067; PIDN:AAA39286.1; PID:
R;Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamura, K.
Biochem. Biophys. Res. Commun. 193, 356-363, 1993
A;Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of functi
A;Reference number: JN0592; MUID:93277575; PMID:8503926
A;Accession: JN0592
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-369 <KUM>
A;Cross-references: UNIPARC:UPI0000001949; DBJ:DJ3565; NID:G303684; PIDN:BAA02760.1; PI
R;Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.
Gene 130, 303-304, 1993
A;Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.
A;Reference number: JN0775; MUID:93366191; PMID:8359699
A;Accession: JN0775
A;Molecule type: mRNA
A;Residues: 1-369 <KOB>
A;Cross-references: UNIPARC:UPI0000001949; GB:DJ3821; NID:G436045; PIDN:BAA02974.1; PID:
R;Chiu, R.K.; Dougherty, G.J.
submitted to the EMBL Data Library, October 1993
A;Description: Regulation of CD44-mediated cellular adhesion by the IL-2 R gamma chain.
A;Reference number: S37582
A;Accession: S37582
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-350,'S',352-366,'S',368-369 <CHI>
A;Cross-references: UNIPARC:UPI0000176753; EMBL:X75337
R;DiSanto, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; Avner, P.; Fischer, A.; de Sa
Eur. J. Immunol. 24, 3014-3018, 1994
A;Title: The murine interleukin-2 receptor gamma chain gene: organization, chromosomal loc
A;Reference number: I53398; MUID:95104285; PMID:7805729
A;Accession: I53398
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-369 <RES>
A;Cross-references: UNIPARC:UPI0000001949; GB:S75852; NID:G861554; PIDN:AAB32904.1; PID:
C;Genetics:
A;Gene: IL-2Rgamma
A;Introns: 39/1, 90/2, 152/1, 199/3, 254/1, 286/2, 308/3
C;Complex: The high affinity receptor is a heterotrimer of alpha (see PIR:UHMS2), beta (se
epitops.
C;Function:
A;Description: receptor for interleukin-2
A;Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, NK ce
C;Superfamily: interleukin-2 receptor gamma chain
C;Keywords: cytokine receptor; duplication; glycoprotein; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-369/Product: interleukin-2 receptor gamma chain #status predicted <MAT>
F;256-284/Domain: transmembrane #status predicted <TMW>
F;71,75,84,96,159,164,306/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 8.9%; Score 205.5; DB 2; Length 369;
Best Local Similarity 24.0%; Pred. No. 2.1e-08;
Matches 76; Conservative 63; Mismatches 121; Indels 57; Gaps 16;
QY 102 STNSEKPSILVEKICSPGDPESAATVTELOCIWNLSYMKCSWLPGRNTSPD---TNYT 158
Db 31 SANEDIKADLIILTSTAPEHLSAFTLPPEVQCFVFNVEYMNCTW---NSSSEFQATNLT 86

159 LYVHRSLEKHQENIFREGQYFGCSFDLTWKVDSPEQHSVO-----IMVKDNAGKI 212
 87 LHYRYKVS-----NNTFQECSHYLFKEIT--SGCQIQKEDIQYQTFVVLQDPKQPKQ 139
 213 KPSFNIPLTSRVKPDPPHINKLSFHN---DDLXVQWENPQNFISRLCFYEVEVNNQTE 269
 140 RRAVQKLNQNLVIRAP--ENLTLNLSQSLELRWKS-RHIKERCQLVLQVRSNRDR 196
 270 THNVFYQAEKACENPEFERNVENTSCFMVPGVLPTLN--TVIRVTKNLCYEDDKLWS 327
 197 SWT-----ELIVNHEPRFSLPSV--DELKRYTFVRVSRYPNPTCGSSQ--WS 239
 328 NWSQEMSGK---KRNSTLYITMLLIVPVIAGAILVLL---YLKRLKILIIFFPIPDGP 381
 240 KWSQFVHWGSHVBNPSLFALEAVLPVGTGMLIITLIFVYCWLERM-----PPIP-PI 293
 382 KIFKEMFGDQNDTLHW 398
 294 KNLDELVTYQGNPSAW 310

RESULT 9
 A:interleukin-2 receptor gamma chain - human
 C:Species: Homo sapiens (man)
 C>Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
 C:Accession: A42565; A46591; I54332
 R:Takeshita, T.; Aseo, H.; Ohtani, K.; Ishii, N.; Kumaki, S.; Tanaka, N.; Munakata, H.; Science 257, 379-382, 1992
 A:Title: Cloning of the gamma chain of the human IL-2 receptor.
 A:Reference number: A42565; MUID:92335983; PMID:1631559
 A:Accession: A42565
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid, protein
 A:Residues: 1-369 <TAK>
 A:Cross-references: UNIPROT:P31785; UNIPARC:UPI0000000DEA; GB:D11086; NID:G303611; PIDN:
 A:Experimental source: MOLT beta lymphoid cells
 A>Note: sequence extracted from NCBI backbone (NCBIP:109167)
 R:Noguchi, M.; Adelstein, S.; Cao, X.; Leonard, W.J.
 J. Biol. Chem. 268, 13601-13608, 1993
 A:Title: Characterization of the human interleukin-2 receptor gamma chain gene.
 A:Reference number: A46591; MUID:93293987; PMID:8514792
 A:Accession: A46591
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-369 <RES>
 A:Cross-references: UNIPARC:UPI0000000DEA; GB:L12183; NID:G307056; PIDN:AAA59145.1; PID:
 R:Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Willard, H.F.; Hum. Mol. Genet. 2, 1099-1104, 1993
 A:Title: The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-linked
 A:Reference number: I54332; MUID:94004847; PMID:8401490
 A:Accession: I54332
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-369 <RE2>
 A:Cross-references: UNIPARC:UPI0000000DEA; GB:L19546; NID:G349631; PIDN:AAC37524.1; PID:
 C:Genetics:
 A:Gene: GDB:IL2RG; SCIDX1; IMD4
 A:Cross-references: GDB:134807; OMIM:308380
 A:Map position: Xq13.1-Xq13.1
 A:introns: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 308/3
 A>Note: defects are associated with an X-linked form of severe combined immunodeficiency
 C:Superfamily: interleukin-2 receptor gamma chain
 C:Keywords: cytokine receptor; duplication; immunodeficiency; transmembrane protein

Query Match 8.7%; Score 202; DB 2; Length 369;
 Best Local Similarity 27.2%; Pred. No. 4e-06;
 Matches 72; Conservative 44; Mismatches 101; Indels 48; Gaps 14;

130 ELQCIWHNLSYMKCSWLPGRNTSPDNTLYYWHRSLS--EKIHQEN-IFREGQYFGCSF 186
 59 EVQCFFVNEVMCTNWSNSRQP-TNLTLLHWYKNSDNDKVKCKSHYLFSEITSGC-- 115

187 DLTKVKDSSPEQHSVOIMVKDNAGKIKPSFNIPLTSRVKPDPPHINKLSFH---NDL 243
 116 QLQKBEHLQYTFVQL--QDPRPRQAQMLKQLNLVIRAP--ENLTLHLKLSQSLE 171
 244 VQWENPQNFISRL---FYEVEVNNQTEHNVFYQAEKACENPEFERNVENTSCFMV 299
 172 LWNVN--RFLNHCLEHLVQYRTDMDHSWT-----EQSDVYRHKFSLP 211
 300 GVLPTDLTNTVIRVTKNLCYEDDKLWSNWSQEMSG---KRNSTLYITMLLIVPVI 356
 212 SVDGQKRYTFVRVSRFNPCLC-GSAQHSWSEHPIHWSNTSKENPFLEAVVISVGS 270
 357 GAILVLL---LYLKRKLKILIIFFPIP 378
 271 GLIISLLCVYFWLER---TMRIP 291

RESULT 10
 JQ1655
 prolactin receptor precursor - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C:Accession: JQ1655
 R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
 Biochem. Biophys. Res. Commun. 188, 490-496, 1992
 A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA se
 A:Reference number: JQ1655; MUID:93075121; PMID:1445292
 A:Accession: JQ1655
 A:Molecule type: mRNA
 A:Residues: 1-831 <TAN>
 A:Cross-references: UNIPROT:Q04594; UNIPARC:UPI0000132232; DBJ:D13154; NID:G222848; PID
 A:Experimental source: kidney
 C:Keywords: glycoprotein; transmembrane protein
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-831/Product: prolactin receptor #status predicted <MAT>
 F:36-219/Domain: cytokine receptor homology <CRS1>
 F:239-425/Domain: cytokine receptor homology <CRS2>
 F:439-462/Domain: transmembrane #status predicted <TM>
 F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (covale

Query Match 8.5%; Score 197.5; DB 2; Length 831;
 Best Local Similarity 23.1%; Pred. No. 2.6e-07;
 Matches 91; Conservative 59; Mismatches 159; Indels 85; Gaps 19;

31 QP--PVTNLSVSVENLCTV--IWT-WNPP--EGASSNCSLWVFSHFQDKQKIAPETRR 83
 126 QPGSFV-NLTLETKRANIMYLWAKWSPLLADASSN---HLVYH----ELRIKPEKE 176
 84 SIEVPLNERICLQVGSQCSTNE-----SEKPSILVEKCI8PP 120
 177 EWET-----ISVGVTQCKINLNAAGMYVQVVRCTLDPGSEWSSESRHILIPSGQSP 231
 121 EGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTLYYWHRSLEKIHQENIFREG 180
 232 E-----KPTIIKCRSPEKETFTCKWPKGLDGGHPNTYTLTYSKEGEEQVYECPD-YRTAG 285
 191 YFGCSFDLTWKVDSPEQHSVOIMVKDNAGKIKPSFNIPLTSRVKPDPP-----HIKNL 235
 286 PNSCYFD--KKHTSFWTIYNITVRATNEMGNSSDPHVVDVTYIVQPPPPVNVTELEK 343
 236 SFHNDLXVQWENPQNFISR---CLFYEVEVNNQTEHNVFYQAEKACENPEFERNV 291
 344 INRKPYLVLTWSPPPPLADVRSGWLTLEVLRLKPEGEWEWTFIVGQ-QTYQKMSLN-- 400
 292 NTSCEPMVGVLPDNLTVIRVTKNLCYEDDKLWSNWSQEMSGIKKRNSTLYITMLLIV 351
 401 -----PGKKYIIQHCKP-----DHHGWSSEWSSENYIQIPNDFRVKDMIVIV 444
 352 PVIVAGAILVLL---LYLKRKLKILIP--PPIPD 380
 445 LGVLSLLCLIMSWTMTVLKGYRMITMLPPVPGP 478

RESULT 11
A34631
lactogen receptor 1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jul-1990 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
C:Accession: A34631
R;Zhang, R.; Buczko, E.; Tsai-Morris, C.H.; Hu, Z.Z.; Dufau, M.L.
Biochem. Biophys. Res. Commun. 168, 415-422, 1990
A:Title: Isolation and characterization of two novel rat ovarian lactogen receptor cDNA
A:Reference number: A34631; MUID:90241201; PMID:2159291
A:Accession: A34631
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-610 <ZHA>
A:Cross-references: UNIPROT:P05710; UNIPARC:UPI0000170BE1; GB:M34083; NID:g205122; PIDN:
F;31-216/Domain: cytokine receptor homology <CRS>

Query Match 8.1%; Score 190; DB 2; Length 610;
Best Local Similarity 23.7%; Pred. No. 6.6e-07;
Matches 68; Conservative 43; Mismatches 120; Indels 56; Gaps 10;

QY 108 KPSILVEKICSPPEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDTNVTLYYHRSLE 167
Db 25 KPEI--HKCRSP---DKET-----FTCWNPFGTDGGLPTNYSLTYSKEGK 65

QY 168 KIHQCNIFREGQYFGCSFDLTAKVDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKP 227
Db 66 TTVECPDYKTSGN-SCFF--SKQYTSIWKIYIITVNATNQMGSSSDPLYVDVTIVPEP 122

QY 228 DPP-----HIKNLSFNDLLYQWENPQNFISR-----CLFYEVVNNSTQETHNVFYVQE 278
Db 123 EPPRNLTLEVKQLKDKKTYLWVKWSPPTITDVKTGFTMEYERLKPPEAEWEIHF--- 179

QY 279 AKCENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYEDDKLWNSWQSEMIGKK 338
Db 180 -----TGHQTFKVFDPYQKYLQVTR-----CKPDHGYWRSWQSESSVEMP 222

QY 339 RNSTLYTMLLIVPVIVAGAIIVLLYLKRLK-----IIFPPPIPP 380
Db 223 NDFTLKDTTWTIIIVAILSAVICLIWVAVALKGYSMMTCIFFPPVPGP 269

RESULT 12
A29884
prolactin receptor precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C:Accession: A29884
R;Boutin, J.M.; Jolicœur, C.; Okamura, H.; Gagnon, J.; Edery, M.; Shirota, M.; Banville
Cell 53, 69-77, 1988
A:Title: Cloning and expression of the rat prolactin receptor, a member of the growth ho
A:Reference number: A29884; MUID:88165059; PMID:2832068
A:Accession: A29884
A:Molecule type: mRNA
A:Residues: 1-310 <BOU>
A:Cross-references: UNIPROT:P05710; UNIPARC:UPI000002B19A; GB:M19304; NID:g206364; PIDN:
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-310/Product: prolactin receptor #status predicted <MAT>
F;31-216/Domain: cytokine receptor homology <CRS>

Query Match 8.1%; Score 189; DB 2; Length 310;
Best Local Similarity 23.7%; Pred. No. 3.3e-07;
Matches 68; Conservative 43; Mismatches 120; Indels 56; Gaps 10;

QY 108 KPSILVEKICSPPEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDTNVTLYYHRSLE 167
Db 25 KPEI--HKCRSP---DKET-----FTCWNPFGTDGGLPTNYSLTYSKEGK 65

QY 168 KIHQCNIFREGQYFGCSFDLTAKVDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKP 227

Db 66 TTVECPDYKTSGN-SCFF--SKQYTSIWKIYIITVNATNQMGSSSDPLYVDVTIVPEP 122
QY 228 DPP-----HIKNLSFNDLLYQWENPQNFISR-----CLFYEVVNNSTQETHNVFYVQE 278
Db 123 EPPRNLTLEVKQLKDKKTYLWVKWSPPTITDVKTGFTMEYERLKPPEAEWEIHF--- 179
QY 279 AKCENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYEDDKLWNSWQSEMIGKK 338
Db 180 -----TGHQTFKVFDPYQKYLQVTR-----CKPDHGYWRSWQSESSVEMP 222
QY 339 RNSTLYTMLLIVPVIVAGAIIVLLYLKRLK-----IIFPPPIPP 380
Db 223 NDFTLKDTTWTIIIVAILSAVICLIWVAVALKGYSMMTCIFFPPVPGP 269

RESULT 13
A41070
prolactin receptor Nb2 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 09-Jul-2004
C:Accession: A41070; I55417
R;Ali, S.; Pellegrini, I.; Kelly, P.A.
J. Biol. Chem. 266, 20110-20117, 1991
A:Title: A prolactin-dependent immune cell line (Nb2) expresses a mutant form of prolactin
A:Reference number: A41070; MUID:92041834; PMID:1718958
A:Accession: A41070
A:Molecule type: mRNA
A:Residues: 1-412 <ALI>
A:Cross-references: UNIPROT:P05710; UNIPARC:UPI000002B19B; GB:M74152; NID:g206389; PIDN:
R;O'Neal, K.D.; Yu-Lee, L.Y.
J. Biol. Chem. 269, 26076-26082, 1994
A:Title: Differential signal transduction of the short, Nb2, and long prolactin receptors
A:Reference number: I55417; MUID:95014432; PMID:7929319
A:Accession: I55417
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-412 <RES>
A:Cross-references: UNIPARC:UPI000002B19B; EMBL:U07567; NID:g641963; PIDN:AAA61784.1; PI
A:Experimental source: Nb2-11C cell line
C:Keywords: transmembrane protein
F;31-216/Domain: cytokine receptor homology <CRS>

Query Match 8.1%; Score 189; DB 2; Length 412;
Best Local Similarity 23.7%; Pred. No. 4.8e-07;
Matches 68; Conservative 43; Mismatches 120; Indels 56; Gaps 10;

QY 108 KPSILVEKICSPPEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDTNVTLYYHRSLE 167
Db 25 KPEI--HKCRSP---DKET-----FTCWNPFGTDGGLPTNYSLTYSKEGK 65

QY 168 KIHQCNIFREGQYFGCSFDLTAKVDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKP 227
Db 66 TTVECPDYKTSGN-SCFF--SKQYTSIWKIYIITVNATNQMGSSSDPLYVDVTIVPEP 122

QY 228 DPP-----HIKNLSFNDLLYQWENPQNFISR-----CLFYEVVNNSTQETHNVFYVQE 278
Db 123 EPPRNLTLEVKQLKDKKTYLWVKWSPPTITDVKTGFTMEYERLKPPEAEWEIHF--- 179

QY 279 AKCENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYEDDKLWNSWQSEMIGKK 338
Db 180 -----TGHQTFKVFDPYQKYLQVTR-----CKPDHGYWRSWQSESSVEMP 222
QY 339 RNSTLYTMLLIVPVIVAGAIIVLLYLKRLK-----IIFPPPIPP 380
Db 223 NDFTLKDTTWTIIIVAILSAVICLIWVAVALKGYSMMTCIFFPPVPGP 269

RESULT 14
A36116
prolactin receptor 2 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C:Accession: A36116

QY 270 THNVFYVQAEAKENPFRNVENTSCPMVPGVLPDTLTNTVRIRVTKTNKLCYEDDDKLGWSN 329

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 21:53:18 ; Search time 148.19 Seconds
(without alignments)
2028.173 Million cell updates/sec

Title: US-10-036-568A-4
Perfect score: 2320
Sequence: 1 MEWPARICGLWALLCAGG.....QTKETDSVVLINLKKASQ 426

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2309.5	99.5	427	1 IL13R1_HUMAN	P78552 homo sapien
2	2309.5	99.5	427	2 Q5U516_XENLA	Q5j6l4 homo sapien
3	2296.5	99.0	427	2 Q96BB4_HUMAN	Q96BB4 homo sapien
4	2291.5	98.8	426	2 Q59EG2_HUMAN	Q59EG2 homo sapien
5	2140	92.2	409	2 Q7YRV5_MACFA	Q7YRV5 macaca fasc
6	1939.5	83.6	423	2 Q863Z6_PIG	Q863Z6 sus scrofa
7	1927	83.1	401	2 Q6U6T1_SHEEP	Q6u6t1 ovis aries
8	1878	80.9	405	2 Q95LPI_CANFA	Q95lfl canis famil
9	1696	73.1	424	1 IL13R1_MOUSE	Q90030 mus musculu
10	1690	72.8	424	2 Q8C1Z3_MOUSE	Q8clz3 mus musculu
11	1687	72.7	426	2 Q561K3_RAT	Q561k3 rattus norv
12	1680	72.4	424	2 Q8BNM4_MOUSE	Q8bnm4 mus musculu
13	1654	71.3	426	2 Q8VHC2_RAT	Q8vhc2 rattus norv
14	1610	69.4	349	2 Q97597_BOVIN	Q97597 bos tauris
15	1524.5	65.7	279	2 Q9UDY5_HUMAN	Q9udy5 homo sapien
16	977.5	42.1	252	2 Q8VDP7_MOUSE	Q8vdp7 mus musculu
17	463	20.0	226	2 Q6ZW70_HUMAN	Q6zw70 homo sapien
18	329	14.2	386	1 IL13R2_CANFA	Q951f0 canis famil
19	318	13.7	415	1 IL13R2_MOUSE	P21183 mus musculu
20	296.5	12.8	420	1 IL13R2_HUMAN	Q01344 homo sapien
21	294.5	12.7	380	1 IL13R2_HUMAN	Q14627 homo sapien
22	294.5	12.7	420	2 Q14633_HUMAN	Q14633 homo sapien
23	287.5	12.4	383	2 Q88786_MOUSE	Q88786 mus musculu
24	282.5	12.2	396	2 Q14631_HUMAN	Q14631 homo sapien
25	279.5	12.0	415	2 Q920K4_CAVPO	Q920k4 cavia porce
26	277	11.9	385	2 Q8VHK6_RAT	Q8vnh6 rattus norv
27	273.5	11.8	414	2 Q920B8_RAT	Q920b8 rattus norv
28	272.5	11.7	448	2 Q99FS3_RAT	Q99fs3 rattus norv
29	269.5	11.6	318	2 Q8AUP2_CHICK	Q8aup2 gallus gall
30	263	11.3	391	2 Q6UAN8_TETNG	Q6uan8 tetraodon n
31	262.5	11.3	374	2 Q8AV07_CHICK	Q8av07 gallus gall

RESULT 1

ID	IL13R1_HUMAN	STANDARD;	PRT;	427 AA.
AC	P78552; Q95646; Q99656;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-13RA-1) (CD213al antigen).			
GN	Name=IL13RA1; Synonyms=IL13R, IL13RA;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Carcinoma;			
RX	MEDLINE=97165986; PubMed=9013879; DOI=10.1016/S0014-5793(96)01462-7;			
RA	Miloux B.; Laurent P.; Bonnin O.; Lupker J.; Caput D.; Vita N.,			
RA	Ferrara P.;			
RT	"Cloning of the human IL-13R alpha chain and reconstitution with the IL4R alpha of a functional IL-4/IL-13 receptor complex.";			
RL	FEBS Lett. 401:163-166(1997).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=B-cell;			
RA	Gauchat J.F.M., Schlagenhaut B., Feng N.P., Moser R., Yanage M.,			
RA	Jeannin P., Alouani S., Elson G., Notarangelo L.D., Wells T.,			
RA	Eugster H.P., Bonnefoy J.Y.;			
RL	Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=T-cell;			
RX	MEDLINE=97067184; PubMed=8910586; DOI=10.1074/jbc.271.46.29265;			
RA	Aman M.J., Tayebi N., Obiri N.I., Puri R.K., Modi W.S., Leonard W.J.;			
RT	"cDNA cloning and characterization of the human interleukin 13 receptor alpha chain.";			
RL	J. Biol. Chem. 271:29265-29270(1996).			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE.			
RC	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.			
RL	Wada M., Hisano T., Kuwano M.;			
RN	[5]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].			
RC	TISSUE=Pancreas;			
RX	MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			

Q5U516 xenopus lae
Q90XP8 oncorhynchu
Q15469 homo sapien
P15509 homo sapien
Q4V311 homo sapien
Q8nhv7 homo sapien
Q4V312 homo sapien
Q66IN1 xenopus lae
Q76kd0 sus scrofa
Q8sq71 sus scrofa
Q68fu6 rattus norv
P40321 canis famil
P43902 mus musculu
Q8vhr8 rattus norv

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- FUNCTION: Binds IL13 with a low affinity. Together with IL4R-alpha
CC can form a functional receptor for IL13. Also serves as an
CC alternate accessory protein to the common cytokine receptor gamma
CC *chain for IL4 signaling, but cannot replace the function of gamma
CC C in allowing enhanced IL2 binding activity.
CC -1- SUBUNIT: Interleukin 13 receptor is a complex of IL4R, IL13RA1,
CC and possibly other components.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Ubiquitous. Highest levels in heart, liver,
CC skeletal muscle and ovary; lowest levels in brain, lung and
CC kidney. Also found in B-cells, T-cells and endothelial cells.
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding.
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation.
CC -1- SIMILARITY: Belongs to the type I cytokine receptor family. Type 5
CC subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; Y10659; CA471669.1; -; mRNA.
DR EMBL; Y09328; CA470508.1; -; mRNA.
DR EMBL; U62858; AAB37127.1; -; mRNA.
DR EMBL; U81379; AAD00510.3; -; mRNA.
DR EMBL; BC009960; AAH09960.1; -; mRNA.
DR Ensembl; ENSG00000131724; Homo sapiens.
DR HGNC; HGNC:5974; IL13RA1.
DR H-InvDB; HIX0017008; -.
DR MIM; 300119; -.
DR GO; GO:0005898; C:interleukin-13 receptor complex; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . . ; TAS.
DR InterPro; IPR002996; P:cell surface receptor linked signal transdu. . . ; TAS.
DR InterPro; IPR003532; Hemtptnrecept_F2.
DR PROSITE; PS01356; HEMATOPO REC S_F2; 1.
KW Glycoprotein; Receptor; Signal; Transmembrane.
FT SIGNAL 1 21 Potential
FT CHAIN 22 427 Interleukin-13 receptor alpha-1 chain.
FT TOPO_DOM 22 343 Extracellular (Potential).
FT TRANSMEM 344 367 Potential.
FT TOPO_DOM 368 427 Cytoplasmic (Potential).
FT MOTIF 327 331 WSXWS motif.
FT MOTIF 374 382 Box 1 motif.
FT CARBOHYD 37 37 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 61 61 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 105 105 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 138 138 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 157 157 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 235 235 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 265 265 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 293 293 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 329 329 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 341 341 N-linked (GlcNAc. . .) (Potential).
FT DISULFID 46 95 Potential.
FT DISULFID 134 144 By similarity.

FT DISULFID 173 185 By similarity.
FT CONFLICT 130 130 T -> I (in Ref. 3).
FT CONFLICT 358 358 G -> D (in Ref. 3).
SQ SEQUENCE 427 AA; 48760 MW; 5983B38BF54107B CRC64;
Query Match 99.5%; Score 2309.5; DB 1; Length 427;
Best Local Similarity 99.8%; Pred. No. 6.1e-167;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MEWPARLCGLWALLLLCAGGGGGG--APTETQPPVTLNLSVSVENLCTVIWTPNPPGASS 59
DB 1 MEWPARLCGLWALLLLCAGGGGGGAAAPTETQPPVTLNLSVSVENLCTVIWTPNPPGASS 60
QY 60 NCSLWTFHFHGDQDKKIAPETRRSIEVPLNERICLVGSGQCSQSTNESEKPSILVEKICISP 119
DB 61 NCSLWTFHFHGDQDKKIAPETRRSIEVPLNERICLVGSGQCSQSTNESEKPSILVEKICISP 120
QY 120 PEGDPESAVTELQCIWHNLNLSYKMSWLPGRNTPDNTYLYWHRSLKIHQCNIFREG 179
DB 121 PEGDPESAVTELQCIWHNLNLSYKMSWLPGRNTPDNTYLYWHRSLKIHQCNIFREG 180
QY 180 QYFGCSFDLTWKVDSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPPDPHHIKNLSFHN 239
DB 181 QYFGCSFDLTWKVDSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPPDPHHIKNLSFHN 240
QY 240 DDLVQWENPQNFISRCIFYEVVNSQTFTHNVFVQVQAKCENPERFERNVENTSCFMPV 299
DB 241 DDLVQWENPQNFISRCIFYEVVNSQTFTHNVFVQVQAKCENPERFERNVENTSCFMPV 300
QY 300 GVLPTLNTVRVTKNKLCYEDDKLWSNWSQMSIGKRNSTLYITMLLIIVPVIAGAI 359
DB 301 GVLPTLNTVRVTKNKLCYEDDKLWSNWSQMSIGKRNSTLYITMLLIIVPVIAGAI 360
QY 360 IVLLLYLKLKLIIPPIPDGKIFKEMFGDQNDTLHWKQDIYKQTKETSDSVLIE 419
DB 361 IVLLLYLKLKLIIPPIPDGKIFKEMFGDQNDTLHWKQDIYKQTKETSDSVLIE 420
QY 420 NLKKSQ 426
DB 421 NLKKSQ 427
RESULT 2
Q5JSL4_HUMAN PRELIMINARY; PRT; 427 AA.
AC Q5JSL4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Interleukin 13 receptor, alpha 1.
GN Names=IL13RA1; ORFNames=RPI3-12804.2-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lawlor S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
DR EMBL; AL391280; CAI41410.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . . ; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytkn_recept_B/G.
DR InterPro; IPR003532; Hemtptnrecept_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.

```
KW Receptor; Transmembrane.
SQ SEQUENCE 427 AA; 48760 MW; 5983B3B8F55A107B CRC64;

Query Match 99.5%; Score 2309.5; DB 2; Length 427;
Best Local Similarity 99.8%; Pred. No. 6.1e-167;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MEWPARLCGLWALLLCAGGGGGG-APTETPPVNTLSVSVENLCTVIWTWNPPEGASS 59
Db 1 MEWPARLCGLWALLLCAGGGGGGAAPTETPPVNTLSVSVENLCTVIWTWNPPEGASS 60

Qy 60 NCSLWYFSGHFGDKQDKKIAPETRRSIEVPLNERICLQVGSQCTNESKPSILVEKICSP 119
Db 61 NCSLWYFSGHFGDKQDKKIAPETRRSIEVPLNERICLQVGSQCTNESKPSILVEKICSP 120

Qy 120 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTTLYYHRSLEKIHOCENIFREG 179
Db 121 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTTLYYHRSLEKIHOCENIFREG 180

Qy 180 QYFGCSPLTKVKDSSFEQHSQVQIMVKNAGKIKPSFNIVPLTSRVKDPDPHIKNLSFHN 239
Db 181 QYFGCSPLTKVKDSSFEQHSQVQIMVKNAGKIKPSFNIVPLTSRVKDPDPHIKNLSFHN 240

Qy 240 DDLYVQWENPQNFISRCILFYEVVNNSTQTHNVFYQEAECENPEFERNVENTSCFMVP 299
Db 241 DDLYVQWENPQNFISRCILFYEVVNNSTQTHNVFYQEAECENPEFERNVENTSCFMVP 300

Qy 300 GVLPTLNTVIRVKTNKLCEYEDDKLWSNQSQMSIGKKNSTLYITMLLIVPVIVAGAI 359
Db 301 GVLPTLNTVIRVKTNKLCEYEDDKLWSNQSQMSIGKKNSTLYITMLLIVPVIVAGAI 360

Qy 360 IVLLLYLRLKLIIPPPIDPKIKPMFGQNDTTLHWKKYDIYEKOTKEETSDSVLIE 419
Db 361 IVLLLYLRLKLIIPPPIDPKIKPMFGQNDTTLHWKKYDIYEKOTKEETSDSVLIE 420

Qy 420 NLKQASQ 426
Db 421 NLKQASQ 427

RESULT 3
Q56BB4 HUMAN
ID Q56BB4 HUMAN PRELIMINARY; PRT; 427 AA.
AC Q56BB4; Q8WX08;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE Interleukin 13 receptor, alpha 1.
GN Name=IL13RA1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon;
RA Strausberg R.;
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- DOMAIN: The WSWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
DR EMBL; BC015768; AHI15768.1; -; mRNA.
DR GO; GO:0016031; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytokn_recept_B/G.
DR InterPro; IPR003532; Hemtptnrecept_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 427 AA; 48677 MW; E6A42F7466A39A09 CRC64;

Query Match 99.0%; Score 2296.5; DB 2; Length 427;
Best Local Similarity 99.5%; Pred. No. 5.9e-166;
Matches 425; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 MEWPARLCGLWALLLCAGGGGGG-APTETPPVNTLSVSVENLCTVIWTWNPPEGASS 59
Db 1 MEWPARLCGLWALLLCAGGGGGGAAPTETPPVNTLSVSVENLCTVIWTWNPPEGASS 60

Qy 60 NCSLWYFSGHFGDKQDKKIAPETRRSIEVPLNERICLQVGSQCTNESKPSILVEKICSP 119
Db 61 NCSLWYFSGHFGDKQDKKIAPETRRSIEVPLNERICLQVGSQCTNESKPSILVEKICSP 120

Qy 120 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTTLYYHRSLEKIHOCENIFREG 179
Db 121 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTTLYYHRSLEKIHOCENIFREG 180

Qy 180 QYFGCSPLTKVKDSSFEQHSQVQIMVKNAGKIKPSFNIVPLTSRVKDPDPHIKNLSFHN 239
Db 181 QYFGCSPLTKVKDSSFEQHSQVQIMVKNAGKIKPSFNIVPLTSRVKDPDPHIKNLSFHN 240

Qy 240 DDLYVQWENPQNFISRCILFYEVVNNSTQTHNVFYQEAECENPEFERNVENTSCFMVP 299
Db 241 DDLYVQWENPQNFISRCILFYEVVNNSTQTHNVFYQEAECENPEFERNVENTSCFMVP 300

Qy 300 GVLPTLNTVIRVKTNKLCEYEDDKLWSNQSQMSIGKKNSTLYITMLLIVPVIVAGAI 359
Db 301 GVLPTLNTVIRVKTNKLCEYEDDKLWSNQSQMSIGKKNSTLYITMLLIVPVIVAGAI 360

Qy 360 IVLLLYLRLKLIIPPPIDPKIKPMFGQNDTTLHWKKYDIYEKOTKEETSDSVLIE 419
Db 361 IVLLLYLRLKLIIPPPIDPKIKPMFGQNDTTLHWKKYDIYEKOTKEETSDSVLIE 420

Qy 420 NLKQASQ 426
Db 421 NLKQASQ 427

RESULT 4
Q59EG2 HUMAN
ID Q59EG2 HUMAN PRELIMINARY; PRT; 426 AA.
AC Q59EG2;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE Interleukin 13 receptor, alpha 1 variant (Fragment).
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Aorta endothelial cell;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB209849; BAD93086.1; -; mRNA.
KW Receptor.
FT CHAIN 1 1
SQ SEQUENCE 426 AA; 48555 MW; 342A3A6F7347261B CRC64;

Query Match 98.8%; Score 2291.5; DB 2; Length 426;
Best Local Similarity 99.5%; Pred. No. 1.4e-165;
Matches 424; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 EWPALCGLWALLLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTPNPPGASSN 60
Db 1 EWPALCGLWALLLCAGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTPNPPGASSN 60
QY 61 CSLWYFSHFCDKQDKIAPETRSIEVPLNERICLVGSCSTNESEKPSILVEKICISPP 120
Db 61 CSLWYFSHFCDKQDKIAPETRSIEVPLNERICLVGSCSTNESEKPSILVEKICISPP 120
QY 121 EGPESAVTELCITWNLSTYMKCSWLPGRNTSPDTNTLYYHRSLEKIHQENIFREGQ 180
Db 121 EGPESAVTELCITWNLSTYMKCSWLPGRNTSPDTNTLYYHRSLEKIHQENIFREGQ 180
QY 181 YFGCSFDLTQKVDSSFEQSHVQIMVKDNAGIKPSFNIVPLTSRVKDPDPHINKLSFHD 240
Db 181 YFGCSFDLTQKVDSSFEQSHVQIMVKDNAGIKPSFNIVPLTSRVKDPDPHINKLSFHD 240
QY 241 DLVVOENPNQFISRCIFYEVEVNNSTQTHNFYVQEAKECENPEFERNVENTSCFVPG 300
Db 241 DLVVOENPNQFISRCIFYEVEVNNSTQTHNFYVQEAKECENPEFERNVENTSCFVPG 300
QY 301 VLPDTLNTVIRVKTNKLCEYDDKLSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIL 360
Db 301 VLPDTLNTVIRVKTNKLCEYDDKLSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIL 360
QY 361 VLLYLKRLKILIFPPIDPGKIFKEMFGQNDTTLHWKYDIYEKOTKEETSDSVLIEN 420
Db 361 VLLYLKRLKILIFPPIDPGKIFKEMFGQNDTTLHWKYDIYEKOTKEETSDSVLIEN 420
QY 421 LKKASQ 426
Db 421 LKKASQ 426

RESULT 5
QYRV5_MACFA
ID QYRV5_MACFA PRELIMINARY; PRT; 409 AA.
AC QYRV5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin 13 receptor alpha 1 (Fragment).
GN Name=IL13RA1;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Maccarone P., Drinkwater C.C., Nash A.D.;
RA "Cynomolgus monkey interleukin 13 receptor alpha 1.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV312267; AAF78901.1; -; mRNA.

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DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytokn_recept_B/G.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003532; Hemtptnrecept_F2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor.
FT CHAIN 9 409 interleukin 13 receptor alpha 1.
FT NON_TER 1 1
SQ SEQUENCE 409 AA; 46685 MW; 9B98A52671686AF4 CRC64;

Query Match 92.2%; Score 2140; DB 2; Length 409;
Best Local Similarity 96.8%; Pred. No. 4.3e-154;
Matches 394; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 19 GGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTPNPPGASSNCLWYFSHFCDKQDKIA 78
Db 2 GGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTPNPPGASSNCLWYFSHFCDKQDKIA 61
QY 79 PETRSIEVPLNERICLVGSCSTNESEKPSILVEKICISPPGDPESAATELCIWHNL 138
Db 62 PETRSIEVPLNEKICLVGSCSTNESEKPSILVEKICISPPGDPESAATELCIWHNL 121
QY 139 SYMKCSWLPGRNTSPDTNTLYYHRSLEKIHQENIFREGQYFGCSFDLTQKVDSSFEQ 198
Db 122 SYMQCSWLPGRNTSPDTNTLYYHRSLEKIROCEEIYKQYFGCSFDLTQKVDSSFEQ 181
QY 199 HSVQIMVKDNAGIKPSFNIVPLTSRVKDPDPHINKLSFHDNLLYVQWENPNQFISRC 258
Db 182 HSVQIMVKDYAGIKPSFNIVPLTSRVKDPDPHINKLSFHDNLLYVQWENPNQFISRC 241
QY 259 YEVEVNNSTQTHNFYVQEAKECENPEFERNVENTSCFVPGVLPDTLNTVIRVKTNKL 318
Db 242 YEVEVNNSTQTHNFVSVQEAKECENPEFERNVENTSCFVPGVLPDTLNTVIRVKTNKL 301
QY 319 CYEDDKLSNWSQMSIGKRNSTLYITMLLIVPVIVAGAILVLLYLKRLKILIFPPIP 378
Db 302 CYEDDKLSNWSQMSIGKRNSTLYITMLLIVPVIVAGAILVLLYLKRLKILIFPPIP 361
QY 379 DPGKIFKEMFGQNDTTLHWKYDIYEKOTKEETSDSVLIENLKKASQ 426
Db 362 DPGKIFKEMFGQNDTTLHWKYDIYEKOTKEETSDSVLIENLKKASQ 409

RESULT 6
Q863Z6_PIG
ID Q863Z6_PIG PRELIMINARY; PRT; 423 AA.
AC Q863Z6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin 13 receptor alpha 1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=15350752; DOI=10.1016/j.vetimm.2004.05.003;
RA Zarbanga D.S., Dawson H., Krangel H., Solano-Aguilar G.,
RA Urban J.F. Jr.;
RT "Molecular cloning of the Swine IL-4 receptor alpha and IL-13 receptor
RT 1-chains; effects of experimental Toxoplasma gondii, Ascaris suum and
RT Trichuris suis infections on tissue mRNA levels.";
RL Vet. Immunol. Immunopathol. 101:223-234 (2004).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC -!- folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or

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SQ SEQUENCE 405 AA; 46328 MW; 926ELIAC7BE5E3F42 CRC64;
Query Match 80.9%; Score 1878; DB 2; Length 405;
Best Local Similarity 85.24; Pred. No. 3.4e-134;
Matches 345; Conservative 24; Mismatches 36; Indels 0; Gaps 0;

QY 22 GGGGAPTETPPVNTLSVSVENLCTVITWNPPEGASSNCISLWVFGHFGDKQDKKIAPET 81
DB 1 GGVAAPTETPPVNTLSVSVENLCTVITWNPPEGASPNCTLYRFGHFGDKQDKKIAPET 60

QY 82 RRSIEVPLNERICLQVGSQCSQSTNESEKPSILVKEKISPPEDGPESAVTELQCIWHNLSYM 141
DB 61 HRSKEVPLNERICLQVGSQCSQSTNESDNPISLVEKCTPPEDGPESAVTELQCVWHNLSYM 120

QY 142 KCSWLPGRNTSPDNTYLYYHRSLEKIHOCENIFREGQVFGCSFDLTKVQDSSPQHSV 201
DB 121 KCTWLPGRNTSPDNTYLYYHRSLSGLKIQCEDIYREGQHIGCSFALTNLKDSSPQHSV 180

QY 202 QIMVKDNAGIKPSFNIVPLTSRVKDDPPHINKLSFHNDLLVYOWENPQNFISRCIFYEV 261
DB 181 QIMVKDNARKIRSFNIVPLTSRVKDDPPHINKLFFQNGLYYVQWKNPQNFISRCIUSYQV 240

QY 262 EVNNSQTEHNVFYOEAKENPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLVE 321
DB 241 EVNNSQTEINDIFYVEAKQNSEFEGNLGTCFMVPGVLPDTLNTVIRVTKNKLVE 300

QY 322 DDKLWNSQEMSIGKRRNSTLYITMLLIVPVTVAGAIIVLLYLKRLKIIIPPTIPDPG 381
DB 301 DDKLWNSQAMSIGENTDPTFTYITMLLATQVIVAGAIIVLLYLKRLKIIIPPTIPDPG 360

QY 382 KIFKEMFGQNDTTLHWKYDIYEKQTKETSDSVLIENLKASQ 426
DB 361 KIFKEMFGQNDTTLHWKYDIYEKQTKETSDSVLIENLKASQ 405

RESULT 9
IL13R1_MOUSE
ID IL13R1_MOUSE STANDARD; PRT; 424 AA.
AC G09030; Q7T727;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-13RA-1) (Interleukin-13 binding protein) (NR4).
DE Names=il13rai; Synonyms=il13r, il13ra;
GN Mus musculus (Mouse).
OS Mus musculus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96133964; PubMed=8552669; DOI=10.1073/pnas.93.1.497;
RA Hilton D.J., Zhang J.-G., Metcalf D., Alexander W.S., Nicola N.A.,
RA Willson T.A.;
RT "Cloning and characterization of a binding subunit of the interleukin 13 receptor that is also a component of the interleukin 4 receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 93:497-501(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=FVB/N; TISSUE=Brain, and Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong I.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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QY 121 EGDPSAVTELOCTWNLNYSKCSWLPGRNTSPDNTYLYTWHRSLKIHOCENIFREGQ 180
 DB 120 EGDPSAVTELOCTWNLNYSKCSWLPGRNTSPDNTYLYTWHRSLKIHOCENIFREGQ 179
 QY 181 YFGSFDLTWKVDSFEQHSQVQIMVKNAGIKFSPNIVPLTSRVPKPPHKNLSFEND 240
 DB 180 HIACSFKLTKV-EPSFEHQVQIMVKNAGIKFSPNIVPLTSRVPKPPHKNLSFEND 238
 QY 241 DLYQWENPQIFSRCLPYEVEVNSQOTETNRVFFVQEAKEPNERPENTSCFVVP 300
 DB 239 ALLVQWKNPQIFSRCLPYEVEVNSQOTETNRVFFVQEAKEPNERPENTSCFVVP 298
 QY 301 VLPDLTVTRVTKNLCYEDDKLWNSQEMSGKGRNSTLYITMLLIVPVLVAGAIL 360
 DB 299 VLADAVYTRVRVTKNLCYEDDKLWNSQEMSGKGRNSTLYITMLLIVPVLVAGAIL 358
 QY 361 VLLYLKRLKLIIFPPDPGKIFKEMFGDQNDTDLHWKCYDIYEKQKBTSDSVLIEN 420
 DB 359 ILLFLKRLKLIIFPPDPGKIFKEMFGDQNDTDLHWKCYDIYEKQKBTSDSVLIEN 418
 QY 421 LKKA 425
 DB 419 LKKA 423

RESULT 10
 Q8C123 MOUSE PRELIMINARY; PRT; 424 AA.
 AC Q8C123
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DE Mus musculus embryo RCB-0549 Cle-H3 cDNA, RIKEN full-length enriched
 DE library, clone:G430044I06 product:interleukin 13 receptor, alpha 1,
 DE full insert sequence.
 GN Name=Il13ral; (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fletschmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Togo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).

RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Embryo;
 RC The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multipipette sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multipipette sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multipipette sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding (By similarity).
 CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation (By similarity).
 CC EMBL; AK099984; BAC1028.1; -; mRNA.
 DR MGI; MGI:105052; Il13ral.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro; IPR002996; Cytokn_recept_B/G.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003532; Hemtptnrecept_F2.
 DR SMART; SM0060; FN3; 1.
 DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
 KW Receptor.
 SQ SEQUENCE 424 AA; 48371 MW; 4B45EB0B76EB83F CRC64;

Query Match 72.8%; Score 1690; DB 2; Length 424;
 Best Local Similarity 74.6%; Pred. No. 7e-120;
 Matches 317; Conservative 40; Mismatches 66; Indels 2; Gaps 2;
 QY 1 MEMPARLCLWALLCAGGGGGGAPTPQPVNTLSVSVENLCTVIWTNPPGASGN 60
 DB 1 MARPALLGELLVLLLTATVGVAAA-TEVQPPVNTLSVSVENLCTVIWTNPPGASPN 59
 QY 61 CSLWTFSPHGDQDKKIAPETRRSIEVPLNERICLVQVSGCSTNSEKPSILVEKICSP 120

RC STRAIN=Fisher F344;
RX MEDLINE=21458304; PubMed=11573960; DOI=10.1006/bbrc.2001.5682;
RA Pierrot C., Beniguel L., Begue A., Khalife J.;

OX	NCBI_TaxID=9913;
[1]	
RN	NUCLEOTIDE SEQUENCE.
RP	MEDLINE=20080132; PubMed=10614495; DOI=10.1016/S0165-2427(99)00117-8;
RX	Trigona W.L., Brown W.C., Estes D.M.;
RA	"Functional implications for signaling via the IL4R/IL13R complex on
RT	bovine cells.";
RL	Vet. Immunol. Immunopathol. 72:73-79 (1999).
RR	EMBL; AF074402; AAC98147.1; -; mRNA.
DR	GO; GO:0016020; C:membrane; IEA.
DR	GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . ; IEA.
DR	GO; GO:0004872; F:receptor activity; IEA.
DR	InterPro; IPR002996; Cytkn_recept_B/G.
DR	InterPro; IPR003532; Hemtptnrcpt_F2.
DR	PROSITE; PS01356; HEMATOP_REC_S_F2; 1.
KW	Receptor.
FT	NON_TER 1 1
PT	NON_TER 349 349
SQ	SEQUENCE 349 AA; 39644 MW; D61A4C918B1940A6 CRC64;
	Query Match 69.4%; Score 1610; DB 2; Length 349;
	Best Local Similarity 84.5%; Pred.No. 6.5e-114;
	Matches 295; Conservative 17; Mismatches 37; Indels 0; Gaps 0;
Qy	34 VTNLSVSVENLCTVIWTNPPEGASNSCLWYFSHFGDKQKKIAPETRRSIEVPLNERI 93
Dd	1 VTNLSVSVENLCTIIWTNPPEGASPCSLKYFSHFGNKQDKKIAPETHRSKEVPLNERI 60
Qy	94 CLOVGSCSTNESEKPSILVEKICSPPEGDPESAATVELQCIIWHNLGYMKCSWLPGRNTPS 153
Dd	61 CLOVGSCSTNESEKPSILVEKICFSPPEGDPESAATVALQCIIWHNLRYMKTWLPGRNASP 120
Qy	154 DTNYLYYHRSLEKHIOHCENIFREGQYFCSCPDLTKVKDSSPEQHSVOIMVKDNAGKIK 213
Dd	121 DPNIYYHNSLGKILQCNFRFGHOITACSNFLTKVKDSSPEQHSVQVMVRDNAGKIS 180
Qy	214 PSFNIVPLTSRVKPDPPPHIKNLSHFHNDLLVQWENPNQFIISRCIFYEVEVNNQSQTTHNV 273
Dd	181 PSFNIVPLTSHVKPDPSHIKNLSHFQNGDLVQWNTNPQNFOSQCLCYEVEVINSHAETHDI 240
Qy	274 FYVQBACENPERPERNVENTSICFWPGVL PDTLTNVTIRVKTNKL CYEDDKLASNWQSEM 333
Dd	241 FYVEEAKCQTEPEGNLEGTCFMVPGVLPDTLTNVTIRVKTNKL CYEDDKLASNWSQAM 300
Qy	334 SICKKENSTLIYTMLIVPVIVAGAIIVALLYLKRLKIIIPPPIDPDK 382
Dd	301 SICGKANQTFIYTLLIPIVIAAVLVLLYLKRLKIIIPPPIDPDK 349
RESULT 15	
Q9UDY5_HUMAN	
ID	Q9UDY5_HUMAN PRELIMINARY; PRT; 279 AA.
AC	Q9UDY5;
DT	01-MAY-2000 (TrEMBLrel. 13, Created)
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT	13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE	Interleukin-13 receptor soluble form (Interleukin 13 receptor, alpha
DE	1).
GN	Names=IL13RA1; ORFNames=RPL13-12804.2-002;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC	Homo.
OX	NCBI_TaxID=9606;
[1]	
RN	NUCLEOTIDE SEQUENCE.
RP	Nucleotide Sequence.
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC	-/- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC	-/- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC	-I- DOMAIN: The WSKWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding (By similarity).
CC	-I- DOMAIN: The box 1 motif is required for JAK interaction and/or activation (By similarity).
DR	EMBL; U61380; AAD0511.2; -; mRNA.
DR	EMBL; AL391280; CA141409.1; -; Genomic DNA.
CG	GO: GO:0016021; C:integral to membrane; IEA.
DR	GO: GO:0016020; C:membrane; IEA.
DR	GO: GO:0004896; F:hematopoietin/interferon-class (D200-domain.. ; IEA.
DR	GO: GO:0004872; F:receptor activity; IEA.
DR	InterPro; IPR002996; Cytkn_recept_B/G.
DR	InterPro; IPR003532; Hemtptnrcpt_F2.
DR	PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW	Receptor; Transmembrane.
SQ	SEQUENCE 279 AA; 31659 MW; E74141FE9F8E9BBB CRC64;
Query Match	65.7%; Score 1524.5; DB 2; Length 279;
Best Local Similarity	99.3%; Pred. No. 1.5e-107;
Matches 276; Conservative	1; Mismatches 0; Indels 1; Gaps
Qy	1 MEWPALCGLWALLLCAGGGGGGGG-APTETQPVTNLVSVENLCTVIWTNPPEGASS 59
Dd	1 MEWPALCGLWALLLCAGGGGGGGGAAPTETQPVTNLVSVENLCTVIWTNPPEGASS 59
Qy	60 NCSLWYFSHFGDKODKKIAPETERSIEVPLNERICIQVGSGCNSESEKPSILVEKCISP 11
Dd	61 NCSLWYFSHFGDKODKKIAPETERSIEVPLNERICIQVGSGCNSESEKPSILVEKCISP 12
Qy	120 PEGDPESAVTELOCIIWHNLSYMKCSWLPGRNTSPDTNYTLYYWRHSLEKHQCENIFREG 17
Dd	121 PEGDPESAVTELOCIIWHNLSYMKCSWLPGRNTSPDTNYTLYYWRHSLEKHQCENIFREG 18
Qy	180 QYFGCSFDLTVKXDSDFEQSHQIVMKDNAGKIKPSFNIVPLTSRVKPPPHIKNLSPFN 23
Dd	181 QYFGCSFDLTVKXDSDFEQSHQIVMKDNAGKIKPSFNIVPLTSRVKPPPHIKNLSPFN 24
Qy	240 DDLYVQWENPNFTISRCLFYEEVYNNSQTETHNVFYVQ 277
Dd	241 DDLYVQWENPNFTISRCLFYEEVYNNSQTETHNVFYVR 278

Search completed: February 8, 2006, 22:05:53
Job time : 152.19 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 22:28:54 ; Search time 115,507 Seconds
(without alignments)
1540.998 Million cell updates/sec

Title: US-10-036-568A-4
Perfect score: 2320
Sequence: 1 MEWPARLCGLWALLCAGGG.....QTKRETDVSVLIENLKKASQ 426

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2309.5	99.5	427	4	US-10-671-697-9
2	2309.5	99.5	427	6	US-11-067-251-3
3	2302.5	99.2	427	5	US-10-850-270-4
4	2302	99.2	426	4	US-10-036-568-4
5	1878	80.9	405	3	US-09-828-995B-50
6	1878	80.9	405	4	US-10-753-159-50
7	1875.5	80.8	780	3	US-09-935-868-34
8	1875.5	80.8	793	3	US-09-313-942-32
9	1875.5	80.8	793	3	US-09-935-868-32
10	1875.5	80.8	793	4	US-10-287-035-32
11	1875.5	80.8	793	4	US-10-282-162-32
12	1875.5	80.8	793	6	US-11-134-114-32
13	1866.5	80.5	780	3	US-09-935-868-42
14	1866.5	80.5	782	3	US-09-935-868-48
15	1865.5	80.4	782	3	US-09-935-868-38
16	1865.5	80.4	782	3	US-09-935-868-52
17	1862	80.3	780	4	US-10-287-035-34
18	1853	79.9	780	4	US-10-287-035-42
19	1853	79.9	782	4	US-10-287-035-48
20	1853	79.8	782	4	US-10-287-035-54
21	1852	79.8	780	4	US-10-287-035-38
22	1852	79.8	782	4	US-10-287-035-52
23	1852	79.8	782	4	US-10-287-035-58
24	1784.5	76.9	664	5	US-10-850-270-10
25	1779.5	76.7	784	3	US-09-313-942-30
26	1779.5	76.7	784	3	US-09-935-868-30
27	1779.5	76.7	784	4	US-10-287-035-30

28	1779.5	76.7	784	4	US-10-282-162-30	Sequence 30, Appl
29	1779.5	76.7	784	6	US-11-134-114-30	Sequence 30, Appl
30	1769	76.2	322	3	US-09-825-561A-82	Sequence 82, Appl
31	1769	76.2	322	5	US-10-872-087-82	Sequence 82, Appl
32	1750	75.4	776	3	US-09-935-868-36	Sequence 36, Appl
33	1741	75.0	776	3	US-09-935-868-44	Sequence 44, Appl
34	1741	75.0	776	4	US-10-287-035-40	Sequence 40, Appl
35	1741	75.0	776	6	US-11-067-251-10	Sequence 10, Appl
36	1741	75.0	776	6	US-11-067-251-12	Sequence 12, Appl
37	1741	75.0	776	6	US-11-067-251-14	Sequence 14, Appl
38	1741	75.0	776	6	US-11-067-251-16	Sequence 16, Appl
39	1740	75.0	776	3	US-09-935-868-46	Sequence 46, Appl
40	1740	75.0	776	3	US-10-287-035-46	Sequence 46, Appl
41	1736	74.8	778	4	US-10-287-035-60	Sequence 60, Appl
42	1736	74.8	778	4	US-10-287-035-60	Sequence 60, Appl
43	1736	74.8	778	3	US-09-935-868-50	Sequence 50, Appl
44	1735	74.8	778	4	US-10-287-035-50	Sequence 50, Appl
45	1735	74.8	778	4	US-10-287-035-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-10-671-697-9
; Sequence 9, Application US/10671697
; Publication No. US20040043921A1
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, JEAN-YVES
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/671,697
; FILING DATE: 29-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/545,002
; FILING DATE: 06-APR-2000
; APPLICATION NUMBER: US 08/969,125
; FILING DATE: 12-NOV-1997
; APPLICATION NUMBER: GB 9625899.1
; FILING DATE: 13-DEC-1996
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 427 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-671-697-9

Query Match 99.5%; Score 2309.5; DB 4; Length 427;
Best Local Similarity 99.8%; Pred. No. 2.6e-188;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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DB 1 MEWPARLCGLWALLCAGGGGGGAAPTETPPVTNLSVSVENLCTVTWTNPPGASS 60
QY 60 NCSLWYFSGHFGDKDKIAPETRRSIEVPLNERICLQVGSQCSTNESEKPSILVEKICISP 119

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Db 121 PEGDPSAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYLYYHRSLEKIHQENIFREG 180
Qy 180 QYFGCSFDLTWKVDSSEFQHSVQIMVKDNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFHN 239
Db 181 QYFGCSFDLTWKVDSSEFQHSVQIMVKDNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFHN 240
Qy 240 DDLYVQWENPQNFISRCLFYEVEVNNSTQETHNVFVYQEAACENPFRNVENTSCFMVP 299
Db 241 DDLYVQWENPQNFISRCLFYEVEVNNSTQETHNVFVYQEAACENPFRNVENTSCFMVP 300
Qy 300 GVLPDPTLNTVIRVKTNKLKYEDDDKLSWNSQBSIGKGRNSTLYITMLLIIVPVIAGAI 359
Db 301 GVLPDPTLNTVIRVKTNKLKYEDDDKLSWNSQBSIGKGRNSTLYITMLLIIVPVIAGAI 360
Qy 360 IVLLLYLKRLLKIIIFPPIDPGKIFKEMFGDQNDTLLHWKKYDIYEKQTKETDSVVLLIE 419
Db 361 IVLLLYLKRLLKIIIFPPIDPGKIFKEMFGDQNDTLLHWKKYDIYEKQTKETDSVVLLIE 420
Qy 420 NLKKSQ 426
Db 421 NLKKSQ 427

RESULT 2
US-11-067-251-3
; Sequence 3, Application US/11067251
; Publication No. US20050191730A1
; GENERAL INFORMATION:
; APPLICANT: Karow, Margaret
; APPLICANT: Fairhurst, Jeanette
; TITLE OF INVENTION: IL-4/IL-13 Specific Polypeptides and Therapeutic Uses Thereof
; FILE REFERENCE: 2020A
; CURRENT APPLICATION NUMBER: US/11/067, 251
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 60/548,541
; PRIOR FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: 60/602,139
; PRIOR FILING DATE: 2004-08-17
; PRIOR APPLICATION NUMBER: 60/628,343
; PRIOR FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapien
; US-11-067-251-3

Query Match 1 99.5% Score 2309.5; DB 6; Length 427;
Best Local Similarity 99.8%; Pred. No. 2.6e-188;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MWPARLCGLWALLLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 59
Db 1 MWPARLCGLWALLLCAGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 60
Qy 60 NCSLWYFSGDKQDKKIAETRRSIEVPLNERICLVGSGQCSNTESEKPSILVEKICSP 119
Db 61 NCSLWYFSGDKQDKKIAETRRSIEVPLNERICLVGSGQCSNTESEKPSILVEKICSP 120
Qy 120 PEGDPSAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYLYYHRSLEKIHQENIFREG 179
Db 121 PEGDPSAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYLYYHRSLEKIHQENIFREG 180
Qy 180 QYFGCSFDLTWKVDSSEFQHSVQIMVKDNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFHN 239
Db 181 QYFGCSFDLTWKVDSSEFQHSVQIMVKDNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFHN 240
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Db 241 DDLYVQWENPQNFISRCLFYEVEVNNSTQETHNVFVYQEAACENPFRNVENTSCFMVP 300
Qy 300 GVLPDPTLNTVIRVKTNKLKYEDDDKLSWNSQBSIGKGRNSTLYITMLLIIVPVIAGAI 359
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Qy 360 IVLLLYLKRLLKIIIFPPIDPGKIFKEMFGDQNDTLLHWKKYDIYEKQTKETDSVVLLIE 419
Db 361 IVLLLYLKRLLKIIIFPPIDPGKIFKEMFGDQNDTLLHWKKYDIYEKQTKETDSVVLLIE 420
Qy 420 NLKKSQ 426
Db 421 NLKKSQ 427
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Qy 240 DDLYVQWENPQNFISRCLFYEVEVNNSTQETHNVFVYQEAACENPFRNVENTSCFMVP 299
Db 241 DDLYVQWENPQNFISRCLFYEVEVNNSTQETHNVFVYQEAACENPFRNVENTSCFMVP 300
Qy 300 GVLPDPTLNTVIRVKTNKLKYEDDDKLSWNSQBSIGKGRNSTLYITMLLIIVPVIAGAI 359
Db 301 GVLPDPTLNTVIRVKTNKLKYEDDDKLSWNSQBSIGKGRNSTLYITMLLIIVPVIAGAI 360
Qy 360 IVLLLYLKRLLKIIIFPPIDPGKIFKEMFGDQNDTLLHWKKYDIYEKQTKETDSVVLLIE 419
Db 361 IVLLLYLKRLLKIIIFPPIDPGKIFKEMFGDQNDTLLHWKKYDIYEKQTKETDSVVLLIE 420
Qy 420 NLKKSQ 426
Db 421 NLKKSQ 427

RESULT 3
US-10-850-270-4
; Sequence 4, Application US/10850270
; Publication No. US20050058645A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd (for all States except the US)
; APPLICANT: Dunlop, Felicity (US only)
; APPLICANT: Baca, Manuel (US only)
; APPLICANT: Nash, Andrew (US only)
; APPLICANT: Fabri, Louis (US only)
; TITLE OF INVENTION: Novel peptides
; FILE REFERENCE: 12175890/EJH
; CURRENT APPLICATION NUMBER: US/10/850,270
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: AU FSI301
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: AU 2003900437
; PRIOR FILING DATE: 2003-02-03
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 427
; TYPE: PRT
; ORGANISM: human
; US-10-850-270-4

Query Match 99.2% Score 2302.5; DB 5; Length 427;
Best Local Similarity 99.5%; Pred. No. 1e-187;
Matches 425; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 MWPARLCGLWALLLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 59
Db 1 MWPARLCGLWALLLCAGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 60
Qy 60 NCSLWYFSGDKQDKKIAETRRSIEVPLNERICLVGSGQCSNTESEKPSILVEKICSP 119
Db 61 NCSLWYFSGDKQDKKIAETRRSIEVPLNERICLVGSGQCSNTESEKPSILVEKICSP 120
Qy 120 PEGDPSAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYLYYHRSLEKIHQENIFREG 179
Db 121 PEGDPSAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYLYYHRSLEKIHQENIFREG 180
Qy 180 QYFGCSFDLTWKVDSSEFQHSVQIMVKDNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFHN 239
Db 181 QYFGCSFDLTWKVDSSEFQHSVQIMVKDNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFHN 240
Qy 240 DDLYVQWENPQNFISRCLFYEVEVNNSTQETHNVFVYQEAACENPFRNVENTSCFMVP 299
Db 241 DDLYVQWENPQNFISRCLFYEVEVNNSTQETHNVFVYQEAACENPFRNVENTSCFMVP 300
Qy 300 GVLPDPTLNTVIRVKTNKLKYEDDDKLSWNSQBSIGKGRNSTLYITMLLIIVPVIAGAI 359
Db 301 GVLPDPTLNTVIRVKTNKLKYEDDDKLSWNSQBSIGKGRNSTLYITMLLIIVPVIAGAI 360
Qy 360 IVLLLYLKRLLKIIIFPPIDPGKIFKEMFGDQNDTLLHWKKYDIYEKQTKETDSVVLLIE 419
Db 361 IVLLLYLKRLLKIIIFPPIDPGKIFKEMFGDQNDTLLHWKKYDIYEKQTKETDSVVLLIE 420
Qy 420 NLKKSQ 426
Db 421 NLKKSQ 427
```

Db 361 IVLLLYLKLKLIIFPPDPGKIFKEMFGDQDDTLHWKKYDIYEKQTEETDSVLLIE 420
Qy 420 NLKASQ 426
| | | | |
Db 421 NLKASQ 427

RESULT 4
US-10-036-568-4
; Sequence 4, Application US/10036568
; Publication No. US20020090682A1
; GENERAL INFORMATION:
; APPLICANT: Willson, Tracy
; APPLICANT: Nicola, Nicos A.
; APPLICANT: Hilton, Douglas J.
; APPLICANT: Metcalfe, Donald
; APPLICANT: Zhang, Jian G.
; TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
; TITLE OF INVENTION: ENCODING SAME
; FILE REFERENCE: Davies cc
; CURRENT APPLICATION NUMBER: US/10/036,568
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US/09/051,843
; PRIOR FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Human IL-13 receptor alpha-chain
US-10-036-568-4

Query Match 99.2%; Score 2302; DB 4; Length 426;
Best Local Similarity 99.3%; Pred. No. 1.1e-187;
Matches 423; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEWPARLCGLWALLICAGGGGGGAPETPTQPPVTNLVSVENLCTVIWNPPEGASSN 60
Db 1 MEWPARLCGLWALLICAGGGGGGAPETPTQPPVTNLVSVENLCTVIWNPPEGASSN 60

Qy 61 CSLWFYSHFGDKQDKKIAPETRRSIEVPLNERICLVGSGQSTNESKPSILVEKICISPP 120
Db 61 CSLWFYSHFGDKQDKKIAPETRRSIEVPLNERICLVGSGQSTNESKPSILVEKICISPP 120

Qy 121 EGDPEAVTELCIWHNLSYMKCWLPGRNTPSDNTNYLYYWHRSLEKIHQENIFREGQ 180
Db 121 EGDPEAVTELCIWHNLSYMKCWLPGRNTPSDNTNYLYYWHRSLEKIHQENIFREGQ 180

Qy 181 YFGCSFDLTQKQSSFEQHSQIWKONAGIKPSFNIVPLTSRVKDPDPHIKNLSFND 240
Db 181 YFGCSFDLTQKQSSFEQHSQIWKONAGIKPSFNIVPLTSRVKDPDPHIKNLSFND 240

Qy 241 DLYVQWENPQNFISRLCYEVEVNNSTQTHNVFVQBAKCNPEFERNVENTSCFMVPG 300
Db 241 DLYVQWENPQNFISRLCYEVEVNNSTQTHNVFVQBAKCNPEFERNVENTSCFMVPG 300

Qy 301 VLPDNLTVIRVTKNKLCEYEDDKLWSNWSQEMSTGKRNSTLYITMLLIVPVIIVAGAI 360
Db 301 VLPDNLTVIRVTKNKLCEYEDDKLWSNWSQEMSTGKRNSTLYITMLLIVPVIIVAGAI 360

Qy 361 VLLYLKRLKLIIFPPDPGKIFKEMFGDQDDTLHWKKYDIYEKQTEETDSVLLIEN 420
Db 361 VLLYLKRLKLIIFPPDPGKIFKEMFGDQDDTLHWKKYDIYEKQTEETDSVLLIEN 420

Qy 421 LKASQ 426
| | | | |
Db 421 LKASQ 426

RESULT 5
US-09-828-995B-50
; Sequence 50, Application US/09828995B
; Patent No. US20020165135A1

; GENERAL INFORMATION:
; APPLICANT: Heska Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13 R
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/09/828,995B
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-828-995B-50

Query Match 80.9%; Score 1878; DB 3; Length 405;
Best Local Similarity 85.2%; Pred. No. 1.7e-151;
Matches 345; Conservative 24; Mismatches 36; Indels 0; Gaps 0;

Qy 22 GGGGAPTETQPPVTNLVSVENLCTVIWNPPEGASNCSLWYFSGDKQDKKIAPET 81
Db 1 GGVAAPTETQPPVTNLVSVENLCTVIWNPPEGASPNCTLRYSFHDNKKKIAPET 60

Qy 82 RRSIEVPLNERICLVGSGQSTNESKPSILVEKICISPPGDPESAVTELCIWHNLSYM 141
Db 61 HRSKEVPLNERICLVGSGQSTNESDNPSPILVEKCTPPGDPESAVTELCQVWHNLSYM 120

Qy 142 KCSWLPGRNTPSDNTNYLYYWHRSLEKIHQENIFREGQYFGCSFDLTQKQSSFEQHSV 201
Db 121 KCTWLPGRNTPSDNTNYLYYWHRSLEKIHQENIFREGQYFGCSFDLTQKQSSFEQHSV 180

Qy 202 QIWKONAGIKPSFNIVPLTSRVKDPDPHIKNLSFNDLIVQWENPQNFISRLCYE 261
Db 181 QIWKONARKIRPSFNIVPLTSRVKDPDPHIKRLFFQGNLYVQWKNPQNFYSRCLSYQV 240

Qy 262 EVNNSQTEHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDNLTVIRVTKNKLCE 321
Db 241 EVNNSQTEHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDNLTVIRVTKNKLCE 300

Qy 322 DDKLWSNWSQEMSTGKRNSTLYITMLLIVPVIIVAGAIIVLLYLKRLKLIIFPPDPG 381
Db 301 DDKLWSNWSQAMSGENTDPTFYITMLLATQVIVAGAIIVLLYLKRLKLIIFPPDPG 360

Qy 382 KIFKEMFGDQDDTLHWKKYDIYEKQTEETDSVLLIENLKASQ 426
Db 361 KIFKEMFGDQDDTLHWKKYDIYEKQTEETDSVLLIENLKASQ 405

RESULT 6
US-10-753-159-50
; Sequence 50, Application US/10753159
; Publication No. US20040142372A1
; GENERAL INFORMATION:
; APPLICANT: Heska Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13 R
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/10/753,159
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 405

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; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-753-159-50

Query Match      80.9%; Score 1878; DB 4; Length 405;
Best Local Similarity 85.2%; Pred. No. 1.7e-151;
Matches 345; Conservative 24; Mismatches 36; Indels 0; Gaps 0;

QY 22 GGGGATETOPPTNLSVSVENLCTVIWTWNPPEGASSNCLWYFHFQDKQDKKIAPET 81
Db 1 GGVAAETETOPPTNLSVSVENLCTVIWTWNPPEGASPNCTLRYFHFQDKQDKKIAPET 60

QY 82 RRSIEVPLNERICLVQVSCSTNESEKPSILVSKCISPPGDPESAVTELQCIWHNLSYM 141
Db 61 HRSKEVPLNERICLVQVSCSTNESONPSILVSKCTPPPEGDPESAVTELQCVWHNLSYM 120

QY 142 KCSWLPGRNTSPDNTNLYYHRSLEKIHOCENIFREGQYFGCSFDLTWKVQDSSFFQHSV 201
Db 121 KCTWLPGRNTSPDNTNLYYHSSLGKILQCEDIYREGQHIGCSFALTNLKQDSSFFQHSV 180

QY 202 QIMVKONAGKIKPSFNIVPLTSRVKDDPPPHIKNLSFHNDLLYQWENPQNFISRCIFYEV 261
Db 181 QIMVKONARKIRPSFNIVPLTSRVKDDPPPHIKRLLFFQGNLYYQWKNPQNFYSRCLSYQV 240

QY 262 EVNNSOTETHNVFVQEAKEENPEERNVENTSCFMVPGVLPDTLNTVRIRVTKNKLQYE 321
Db 241 EVNNSOTETNDIFVYBEAKCONSEFEGNLEGTCFMVPGVLPDTLNTVRIRVTKNKLQYE 300

QY 322 DDKLSNWSQEMSIGKRRNSTLVTMLLIVPVIVAGAILVLLYLKRLKIIIPPIPDGP 381
Db 301 DDKLSNWSQAMSIGENTDPTFTVITMLLATQVIVAGAILVLLYLKRLKIIIPPIPDGP 360

QY 382 KIPKEMFGQNDTTLHWKVDIYEKQTEBTSVLIENLKQAS 426
Db 361 KIPKEMFGQNDTTLHWKVDIYEKQTEBTSVLIENLKQAS 405

RESULT 7
US-09-935-868-34
; Sequence 34, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 34
; LENGTH: 780
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-935-868-34

Query Match      80.8%; Score 1875.5; DB 3; Length 780;
Best Local Similarity 99.4%; Pred. No. 6.6e-151;
Matches 341; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MEWPARGLWALLLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 59
Db 1 MWPARGLWALLLCAGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 60

QY 60 NCSLWYFHFQDKQDKKIAPETRRSIEVPLNERICLVQVSCSTNESEKPSILVEKICIS 119
Db 61 NCSLWYFHFQDKQDKKIAPETRRSIEVPLNERICLVQVSCSTNESEKPSILVEKICIS 120

QY 120 PEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDNTNLYYHRSLEKIHOCENIFREG 179
Db 121 PEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDNTNLYYHRSLEKIHOCENIFREG 180

QY 180 QYFGCSFDLTWKVQDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHN 239
Db 181 QYFGCSFDLTWKVQDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHN 240

QY 240 DDLYQWENPQNFISRCIFYEVENNSQTEETHNVFVQEAKEENPEERNVENTSCFMV 299
Db 241 DDLYQWENPQNFISRCIFYEVENNSQTEETHNVFVQEAKEENPEERNVENTSCFMV 300

QY 300 GVLPTDLTNTVRIRVTKNKLQYEDDKLSNWSQEMSIGKRRNST 342
Db 301 GVLPTDLTNTVRIRVTKNKLQYEDDKLSNWSQEMSIGKRRNST 343

RESULT 8
US-09-313-942-32
; Sequence 32, Application US/09313942
; Publication No. US20020012962A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-32

Query Match      80.8%; Score 1875.5; DB 3; Length 793;
Best Local Similarity 99.4%; Pred. No. 6.8e-151;
Matches 341; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MEWPARGLWALLLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 59
Db 1 MWPARGLWALLLCAGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 60

QY 60 NCSLWYFHFQDKQDKKIAPETRRSIEVPLNERICLVQVSCSTNESEKPSILVEKICIS 119
Db 61 NCSLWYFHFQDKQDKKIAPETRRSIEVPLNERICLVQVSCSTNESEKPSILVEKICIS 120

QY 120 PEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDNTNLYYHRSLEKIHOCENIFREG 179
Db 121 PEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDNTNLYYHRSLEKIHOCENIFREG 180

QY 180 QYFGCSFDLTWKVQDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHN 239
Db 181 QYFGCSFDLTWKVQDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHN 240

QY 240 DDLYQWENPQNFISRCIFYEVENNSQTEETHNVFVQEAKEENPEERNVENTSCFMV 299
Db 241 DDLYQWENPQNFISRCIFYEVENNSQTEETHNVFVQEAKEENPEERNVENTSCFMV 300

QY 300 GVLPTDLTNTVRIRVTKNKLQYEDDKLSNWSQEMSIGKRRNST 342
Db 301 GVLPTDLTNTVRIRVTKNKLQYEDDKLSNWSQEMSIGKRRNST 343

RESULT 9
US-09-935-868-32
; Sequence 32, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
```

		CURRENT APPLICATION NUMBER: US/09/935,868			
		CURRENT FILING DATE: 2002-04-11			
		PRIOR APPLICATION NUMBER: PCT/US99/22045			
		PRIOR FILING DATE: 1999-09-22			
		NUMBER OF SEQ ID NOS: 52			
		SOFTWARE: PatentIn version 3.0			
		SEQ ID NO 32			
		LENGTH: 793			
		TYPE: PRT			
		ORGANISM: Homo sapiens			
		US-09-935-868-32			
		Query Match 80.8%; Score 1875.5; DB 3; Length 793;			
		Best Local Similarity 99.4%; Pred. No. 6.8e-151;			
		Matches 341; Conservative 0; Mismatches 1; Indels 1; Gaps 1;			
QY	1	MWPARLCGLWALLLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTPNPEGASS	59		
Db	1	MWPARLCGLWALLLCAGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTPNPEGASS	60		
QY	60	NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLOVGSQCSTNESEKPSILVEKICIS	119		
Db	61	NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLOVGSQCSTNESEKPSILVEKICIS	120		
QY	120	PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDTNTLYYWHRSLEKIHQENIFREG	179		
Db	121	PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDTNTLYYWHRSLEKIHQENIFREG	180		
QY	180	QYFGCSFDLTTKVXDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHN	239		
Db	181	QYFGCSFDLTTKVXDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHN	240		
QY	240	DDLWQWENPQNFISRCIFYEVEVNNSTQTHNVFYVQEAACENPEFERNVENTSCFMVP	299		
Db	241	DDLWQWENPQNFISRCIFYEVEVNNSTQTHNVFYVQEAACENPEFERNVENTSCFMVP	300		
QY	300	GVLPTLTNTVRIKVTNKLCEYDDKLSWNSQEMSIGKKNST	342		
Db	301	GVLPTLTNTVRIKVTNKLCEYDDKLSWNSQEMSIGKKNST	343		
RESULT 11					
US-10-282-162-32					
; Sequence 32, Application US/10282162					
; Publication No. US20030143697A1					
; GENERAL INFORMATION:					
; APPLICANT: REGENERON PHARMACEUTICALS, INC.					
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING					
; FILE REFERENCE: REG 203-B-US					
; CURRENT APPLICATION NUMBER: US/10/282,162					
; PRIOR FILING DATE: 2002-10-28					
; PRIOR APPLICATION NUMBER: 09/787,835					
; PRIOR FILING DATE: 1999-09-22					
; PRIOR APPLICATION NUMBER: PCT/US99/22045					
; PRIOR FILING DATE: 1999-09-22					
; NUMBER OF SEQ ID NOS: 56					
; SOFTWARE: FastSeq for Windows Version 3.0					
; SEQ ID NO 32					
; LENGTH: 793					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
US-10-282-162-32					
		Query Match 80.8%; Score 1875.5; DB 4; Length 793;			
		Best Local Similarity 99.4%; Pred. No. 6.8e-151;			
		Matches 341; Conservative 0; Mismatches 1; Indels 1; Gaps 1;			
QY	1	MWPARLCGLWALLLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTPNPEGASS	59		
Db	1	MWPARLCGLWALLLCAGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTPNPEGASS	60		
QY	60	NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLOVGSQCSTNESEKPSILVEKICIS	119		
Db	61	NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLOVGSQCSTNESEKPSILVEKICIS	120		
QY	120	PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDTNTLYYWHRSLEKIHQENIFREG	179		
Db	121	PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDTNTLYYWHRSLEKIHQENIFREG	180		
QY	180	QYFGCSFDLTTKVXDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHN	239		
Db	181	QYFGCSFDLTTKVXDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHN	240		
QY	240	DDLWQWENPQNFISRCIFYEVEVNNSTQTHNVFYVQEAACENPEFERNVENTSCFMVP	299		
Db	241	DDLWQWENPQNFISRCIFYEVEVNNSTQTHNVFYVQEAACENPEFERNVENTSCFMVP	300		
QY	300	GVLPTLTNTVRIKVTNKLCEYDDKLSWNSQEMSIGKKNST	342		
Db	301	GVLPTLTNTVRIKVTNKLCEYDDKLSWNSQEMSIGKKNST	343		
RESULT 10					
US-10-287-035-32					
; Sequence 32, Application US/10287035					
; Publication No. US20030104567A1					
; GENERAL INFORMATION:					
; APPLICANT: Neil Stahl and George D. Yancopoulos					
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING					
; FILE REFERENCE: REG 203DA					
; CURRENT APPLICATION NUMBER: US/10/287,035					
; CURRENT FILING DATE: 2002-11-01					
; PRIOR APPLICATION NUMBER: US99/935,868					
; PRIOR FILING DATE: 2001-08-23					
; PRIOR APPLICATION NUMBER: US99/787,835					
; PRIOR FILING DATE: 2001-03-22					
; PRIOR APPLICATION NUMBER: US99/313,942					
; PRIOR FILING DATE: 1999-05-19					
; PRIOR APPLICATION NUMBER: 09/313,942					
; PRIOR FILING DATE: 1999-05-19					
; PRIOR APPLICATION NUMBER: 60/101,858					
; PRIOR FILING DATE: 1998-09-25					
; NUMBER OF SEQ ID NOS: 60					
; SOFTWARE: FastSeq for Windows Version 3.0					
; SEQ ID NO 32					
; LENGTH: 793					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
US-10-287-035-32					
		Query Match 80.8%; Score 1875.5; DB 4; Length 793;			
		Best Local Similarity 99.4%; Pred. No. 6.8e-151;			
		Matches 341; Conservative 0; Mismatches 1; Indels 1; Gaps 1;			

QY 300 GVLPTLTNTVIRVKTNKLCEYDDKLWSNQMSIGKKRNST 342
Db 301 GVLPTLTNTVIRVKTNKLCEYDDKLWSNQMSIGKKRNST 343

RESULT 12

US-11-134-114-32
; Sequence 32, Application US/111134114
; Publication No. US20050222033A1
; GENERAL INFORMATION:
; APPLICANT: Stahl, Neil
; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: Receptor Based Antagonists and Methods of Making and Using
; FILE REFERENCE: 203C1
; CURRENT APPLICATION NUMBER: US/11/134,114
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-114-32

Query Match 80.8%; Score 1875.5; DB 6; Length 793;
Best Local Similarity 99.4%; Pred. No. 6.8e-151;
Matches 341; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MWPARLCGLWALLLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTNPPPEGASS 59
Db 1 MWPARLCGLWALLLCAGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTNPPPEGASS 60
QY 60 NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICIQVGSQCSTNESEKPSILVEKICIS 119
Db 61 NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICIQVGSQCSTNESEKPSILVEKICIS 120
QY 120 PEGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDNTYTYWHRSLKIHQOCENIFREG 179
Db 121 PEGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDNTYTYWHRSLKIHQOCENIFREG 180
QY 180 QYFGCSFDLTQVSDSSFEQHSQVIMVKDNAGIKPSFNIVPLTSRVKPPPHIKNLSFHN 239
Db 181 QYFGCSFDLTQVSDSSFEQHSQVIMVKDNAGIKPSFNIVPLTSRVKPPPHIKNLSFHN 240
QY 240 DDLYQWENPQNFISRCLFYEVEVNNSTETHNVFVQEAKECPENPERVENTSCFMVP 299
Db 241 DDLYQWENPQNFISRCLFYEVEVNNSTETHNVFVQEAKECPENPERVENTSCFMVP 300
QY 300 GVLPTLTNTVIRVKTNKLCEYDDKLWSNQMSIGKKRNST 342
Db 301 GVLPTLTNTVIRVKTNKLCEYDDKLWSNQMSIGKKRNST 343

RESULT 13

US-09-935-868-42
; Sequence 42, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11

; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 780
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-935-868-42

Query Match 80.5%; Score 1866.5; DB 3; Length 780;
Best Local Similarity 99.1%; Pred. No. 3.9e-150;
Matches 340; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MWPARLCGLWALLLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTNPPPEGASS 59
Db 1 MWPARLCGLWALLLCAGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTNPPPEGASS 60
QY 60 NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICIQVGSQCSTNESEKPSILVEKICIS 119
Db 61 NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICIQVGSQCSTNESEKPSILVEKICIS 120
QY 120 PEGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDNTYTYWHRSLKIHQOCENIFREG 179
Db 121 PEGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDNTYTYWHRSLKIHQOCENIFREG 180
QY 180 QYFGCSFDLTQVSDSSFEQHSQVIMVKDNAGIKPSFNIVPLTSRVKPPPHIKNLSFHN 239
Db 181 QYFGCSFDLTQVSDSSFEQHSQVIMVKDNAGIKPSFNIVPLTSRVKPPPHIKNLSFHN 240
QY 240 DDLYQWENPQNFISRCLFYEVEVNNSTETHNVFVQEAKECPENPERVENTSCFMVP 299
Db 241 DDLYQWENPQNFISRCLFYEVEVNNSTETHNVFVQEAKECPENPERVENTSCFMVP 300
QY 300 GVLPTLTNTVIRVKTNKLCEYDDKLWSNQMSIGKKRNST 342
Db 301 GVLPTLTNTVIRVKTNKLCEYDDKLWSNQMSIGKKRNST 343

RESULT 14

US-09-935-868-48
; Sequence 48, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
; LENGTH: 782
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-935-868-48

Query Match 80.5%; Score 1866.5; DB 3; Length 782;
Best Local Similarity 99.1%; Pred. No. 3.9e-150;
Matches 340; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MWPARLCGLWALLLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTNPPPEGASS 59
Db 1 MWPARLCGLWALLLCAGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTNPPPEGASS 60
QY 60 NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICIQVGSQCSTNESEKPSILVEKICIS 119
Db 61 NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICIQVGSQCSTNESEKPSILVEKICIS 120
QY 120 PEGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDNTYTYWHRSLKIHQOCENIFREG 179

Db 121 PEGDPESAVTELCQIWHNLSYMKCSWLPGRNTSPDTNTLYYHRSLEKIHQECENIFREG 180
QY 180 QYFGCSFDLTWKVDSSFEQHSVOIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHN 239
Db 181 QYFGCSFDLTWKVDSSFEQHSVOIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHN 240
QY 240 DDLYVQWENPQNFISRCIFYEVEVNNSTETHNVFYVQEAECENPEFERNVENTSCFMVP 299
Db 241 DDLYVQWENPQNFISRCIFYEVEVNNSTETHNVFYVQEAECENPEFERNVENTSCFMVP 300
QY 300 GVLPTLTNTVIRVKTINKLCYEDDDKLSNWSQEMSIGKKRNST 342
Db 301 GVLPTLTNTVIRVKTINKLCYEDDDKLSNWSQEMSIGKKRNST 343

RESULT 15
US-09-935-868-38
; Sequence 38, Application US/09935868
; Patent No. US2002016490A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 780
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-935-868-38

Query Match 80.4%; Score 1865.5; DB 3; Length 780;
Best Local Similarity 99.1%; Pred. No. 4.7e-150;
Matches 340; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MEWPARLCGLWALLCAGGGGGGGG-APTETOPPVTNLSVSVENLCTVIWNPPEGASS 59
Db 1 MEWPARLCGLWALLCAGGGGGGGGAAPTETQPPVTNLSVSVENLSTVIWNPPEGASS 60
QY 60 NCSLMYFSHFPGDKDKKIAPETRRSIEVPLNERICLVGSCQSTNESEKPSILVEKCI 119
Db 61 NCSLMYFSHFPGDKDKKIAPETRRSIEVPLNERICLVGSCQSTNESEKPSILVEKCI 120
QY 120 PEGDPESAVTELCQIWHNLSYMKCSWLPGRNTSPDTNTLYYHRSLEKIHQECENIFREG 179
Db 121 PEGDPESAVTELCQIWHNLSYMKCSWLPGRNTSPDTNTLYYHRSLEKIHQECENIFREG 180
QY 180 QYFGCSFDLTWKVDSSFEQHSVOIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHN 239
Db 181 QYFGCSFDLTWKVDSSFEQHSVOIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHN 240
QY 240 DDLYVQWENPQNFISRCIFYEVEVNNSTETHNVFYVQEAECENPEFERNVENTSCFMVP 299
Db 241 DDLYVQWENPQNFISRCIFYEVEVNNSTETHNVFYVQEAECENPEFERNVENTSCFMVP 300
QY 300 GVLPTLTNTVIRVKTINKLCYEDDDKLSNWSQEMSIGKKRNST 342
Db 301 GVLPTLTNTVIRVKTINKLCYEDDDKLSNWSQEMSIGKKRNST 343

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 22:29:50 : Search time 9.28509 Seconds
(without alignments)
602.062 Million cell updates/sec

Title: US-10-036-568A-4
Perfect score: 2320
Sequence: 1 MEMPALCGLWALLCAGGG.....OTKETDSVLIENLKASQ 426

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US12_NEW_PUB pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No! is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2309.5	99.5	427	US-11-185-230-4	Sequence 4, Appli
2	1687	72.7	424	US-11-185-230-6	Sequence 6, Appli
3	296.5	12.8	420	US-11-185-230-5	Sequence 5, Appli
4	294.5	12.7	380	US-10-989-313-4	Sequence 4, Appli
5	294.5	12.7	380	US-11-185-230-2	Sequence 2, Appli
6	293.5	12.7	378	US-11/185	Sequence 12, Appli
7	287.5	12.4	383	US-10-989-313-2	Sequence 2, Appli
8	230	9.9	313	US-11-193-512-106	Sequence 106, App
9	202	8.7	341	US-10-511-722-21	Sequence 21, Appli
10	202	8.7	357	US-10-511-722-20	Sequence 20, Appli
11	202	8.7	369	US-11-105-268-60	Sequence 60, Appli
12	178.5	7.7	411	US-11-075-351-47	Sequence 47, Appli
13	173	7.5	646	US-10-995-561-695	Sequence 695, App
14	173	7.5	708	US-10-636-320-2	Sequence 2, Appli
15	173	7.5	918	US-10-995-561-696	Sequence 696, App
16	168.5	7.3	329	US-10-995-561-694	Sequence 694, App
17	168	7.2	897	US-11-124-367A-449	Sequence 449, App
18	168	7.2	897	US-11-124-367A-451	Sequence 451, App
19	166	7.2	903	US-11-124-367A-450	Sequence 450, App
20	125	5.4	825	US-10-995-561-679	Sequence 679, App
21	125	5.4	825	US-11-124-367A-469	Sequence 469, App
22	125	5.4	852	US-11-104-923A-5	Sequence 5, Appli
23	118	5.1	521	US-11-105-268-58	Sequence 58, Appli
24	113	4.9	631	US-10-813-646-22	Sequence 22, Appli
25	111.5	4.8	979	US-10-636-320-6	Sequence 6, Appli

Sequence 3, Appli
Sequence 1687, Ap
Sequence 8, Appli
Sequence 44, Appli
Sequence 3, Appli
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Sequence 2, Appli
Sequence 4, Appli
Sequence 539, App
Sequence 60, Appli
Sequence 7, Appli
Sequence 40, Appli
Sequence 7, Appli
Sequence 29, Appli
Sequence 38, Appli
Sequence 1559, Ap
Sequence 59, Appli
Sequence 2, Appli
Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-11-185-230-4
; Sequence 4, Application US/11185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: INV924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 427
; TYPE: PRT 3
; ORGANISM: Homo sapiens
; FEATURE:
US-11-185-230-4

Query Match	99.5%	Score	2309.5	DB 7	Length	427
Best Local Similarity	99.8%	Pred. No.	1.3e-196			
Matches	426	Conservative	0	Mismatches	0	Indels 1; Gaps 1;
QY	1	MEMPALCGLWALLCAGGGGGGGG-APTETQPPVTNLSVSVENLCTVITWNPPEGASS	59			
Db	1	MEMPALCGLWALLCAGGGGGGGGAAPTETQPPVTNLSVSVENLCTVITWNPPEGASS	60			
QY	60	NCCLWYFSGHFGDKDKKTAPEPTRRSIEVPLNERICLOVGSQCSNESEKPSILVEKICISP	119			
Db	61	NCCLWYFSGHFGDKDKKTAPEPTRRSIEVPLNERICLOVGSQCSNESEKPSILVEKICISP	120			
QY	120	PGSDPESAVTELCQCIWHNLSYMKCSWLPGRNTSPDNTYLYYWHRSLEKIHQCENIFREG	179			
Db	121	PGSDPESAVTELCQCIWHNLSYMKCSWLPGRNTSPDNTYLYYWHRSLEKIHQCENIFREG	180			
QY	180	QYFGCSFDLTVKVDSSEFQHSVQIMVKDNAGIKPSFNIVPLTSRVKPPPHIKNLSFHN	239			
Db	181	QYFGCSFDLTVKVDSSEFQHSVQIMVKDNAGIKPSFNIVPLTSRVKPPPHIKNLSFHN	240			
QY	240	DDLYQWENPQNFISRCIFYEVEVNNISQTEHNVFVQEAACENPFERNVENTSCFMPV	299			
Db	241	DDLYQWENPQNFISRCIFYEVEVNNISQTEHNVFVQEAACENPFERNVENTSCFMPV	300			

QY 300 GVLPTDNTVIRVKTNKLCEYDDKLSNWSQEMSIGKRNSTLYITMLLIVPVIVAGAI 359
Db 301 GVLPTDNTVIRVKTNKLCEYDDKLSNWSQEMSIGKRNSTLYITMLLIVPVIVAGAI 360
QY 360 IVLLLYLRLKLIIFPPIDPGKIFKEMFGDQNDTTLHWKKYDIYKQTKETDSVVLIE 419
Db 361 IVLLLYLRLKLIIFPPIDPGKIFKEMFGDQNDTTLHWKKYDIYKQTKETDSVVLIE 420
QY 420 NLKASQ 426
Db 421 NLKASQ 427
RESULT 2
US-11-185-230-6
; Sequence 6, Application US/11185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 424
; TYPE: PRT 3
; ORGANISM: Mus musculus
; FEATURE:
US-11-185-230-6

Query Match 72.7%; Score 1687; DB 7; Length 424;
Best Local Similarity 74.6%; Pred. No. 1.3e-141;
Matches 317; Conservative 40; Mismatches 66; Indels 2; Gaps 2;
QY 1 MEWPARLCGLWALLCAGGGGGGAPTETQPPVTNLSVSNLCVTIWTNPPGASSN 60
Db 1 MARPALLGELLVLLLTATVGVAAA-TEVQPPVTNLSVSNLCVTIWTNPPGASSN 59
QY 61 CSLWYFHFHGDQDKKIAPETRRSIEVPLNERICLVGSGCSTNESEKPSILVEKICISPP 120
Db 60 CTLRYFHFHDDQDKKIAPETRRKELPLDEKICLVGSGCSTNESEKPSILVEKICISPP 119
QY 121 EGDPEAVTELCIWHNLSYMKCSWLPGRNTSPDTNLTLYWHSLEKIHQENIFREGQ 180
Db 120 EGDRESAVTELCIWHNLSYMKCSWLPGRNTSPDTNLTLYWHSLEKIHQENIFREGQ 179
QY 181 YFGCSFDLTVKDSSPEHSHVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFND 240
Db 180 HIACSFALTKV-BPSFHFQNVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFND 238
QY 241 DLYVQWENPQNFISRCFLFYEVVNNSTETHNFFVQEAKECENPEFERNVENTSCFMVPG 300
Db 239 ALLVQWKNPQNFISRCFLFYEVVNNSTETHNFFVQEAKECENPEFERNVENTSCFMVPG 298
QY 301 VLPDNTLVIRVKTNKLCEYDDKLSNWSQEMSIGKRNSTLYITMLLIVPVIVAGAI 360
Db 299 VLADAVYTVRVRVKTNKLCEYDDKLSNWSQEMSIGKRNSTLYITMLLIVPVIVAGAI 358
QY 361 VLLLYLRLKLIIFPPIDPGKIFKEMFGDQNDTTLHWKKYDIYKQTKETDSVVLIE 420
Db 359 ILFLYLRKLIIFPPIDPGKIFKEMFGDQNDTTLHWKKYDIYKQTKETDSVVLIE 418
QY 421 LKXAS 425
Db 419 LKXAA 423

RESULT 3
US-11-185-230-5
; Sequence 5, Application US/11185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 420
; TYPE: PRT 3
; ORGANISM: Homo sapiens
; FEATURE:
US-11-185-230-5
Query Match 12.8%; Score 296.5; DB 7; Length 420;
Best Local Similarity 24.8%; Pred. No. 9.3e-19;
Matches 102; Conservative 65; Mismatches 180; Indels 65; Gaps 16;
QY 32 PPVTNLSVSNLCVTIWTNPP-PEGASSNCSLWYFHFHGDQDKKIAPETRRSIEVPLN 90
Db 32 PPV-NFTIKVTGLAQVLLQWKPNPDQEQRNVLLEY-----QVKINAPK-EDDYETRI 82
QY 91 ERICLVQV-----GSCQSTNESEKPSILVEKICIS-----PPEGDPESAVTELCIWHNL--- 138
Db 83 ESKCVTILHKGPSASVRTILQNDHSLASSWASAEHLHAPGPSPTSVNLCTTTTNTEDN 142
QY 139 -----SY-----MKCSWLPGRNTSPDTNLTLYWHSLEKIHQENIFRE--QVYFGCSFDL 188
Db 143 YSLRSYQVSLHCTWLVGTDAEDTQYFLYRYGWSWTE--ECQEYSKDTLGRNIACWFFR 200
QY 189 TKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFNDLIVQWEN 248
Db 201 TFLSKGRDWLSVLVNGSKHSIAIRFDQLFALHAIQINPLNLTVAIEGTLSIQWEK 260
QY 249 PQN-FISRCFLFYEVVNNSTETHNFFVQEAKECENPEFERNVENTSCFMVPGVLPDTLN 307
Db 261 PVSAPFIHCFDYEVKIHNTNG-----YLQIEKLTNAFTSIIDLSKY----- 304
QY 308 TVRIRVKTNKLCEYDDKLSNWSQEMSIGKRNSTLYITMLLIVPVIVAGAIIVLLLYLK 367
Db 305 DVQVRAAVSSMCREAG-LMSNSQPIYVGNDEHKPLREWFVIVIMATICIFILISLICK 363
QY 368 --RLKIIIPPIPDGKIFKEMFGDQNDTTLHWKKYDIYKQTKETDSVVL 417
Db 364 ICHLWIKLPPPIPAKSNIKDLFVTN-----YEKAGSSETEIEVI 404
RESULT 4
US-10-989-313-4
; Sequence 4, Application US/10989313
; Publication No. US20050277126A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lora
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; APPLICANT: Wills-Karp, Marsha
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: Cytokine Receptor Chain
; FILE REFERENCE: GI 5268A

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; CURRENT APPLICATION NUMBER: US/10/989,313
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US/09/868,123
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-989-313-4

Query Match      12.7%; Score 294.5; DB 6; Length 380;
Best Local Similarity 27.0%; Pred. No. 1.2e-18;
Matches 100; Conservative 59; Mismatches 138; Indels 73; Gaps 20;

Qy 51 WNPPEGAS--SNCSLWYFSHFQDKQDKKIAPETRISI-----EVLNERICLQVGS 99
Db 53 WQPLSLDHFKECTVEY-----ELKYRNIGSETWTKIITKNLHYKDGFDLKNKIEAKIHT 107

Qy 100 -----QCSNTESEKPSILVEKC--ISPPGDDPESAVTELOCIWHNLSYMKCSWLPGRNTSP 153
Db 108 LLPWQC--TNGSEVQSSWAETTYWIS--PQIGIPETKVQDMDCVYNNWQYLLCSWKPFGIGVLL 165

Qy 154 DTNNTLYYWHRSLEKIHQC--ENIPREGOVFGSPDLTKVKDSSFEQHSVQIMVKDNAGKI 212
Db 166 DTNNTLYYWHRSLEKIHQC--ENIPREGOVFGSPDLTKVKDSSFEQHSVQIMVKDNAGKI 212

Qy 213 KPSEFNIVPLTSRVKPPPHIKNLSFHNH---DLVYQWENPQNF1--SRCLFYEVEVNNST 268
Db 224 RSYFTFQQLQNVKPLPP--VYLTFRESSCEIKLWSIPLGPIPARCFDYEIREDDT 281

Qy 269 ETHNVFYVQEAECNPEFERNVENTS---CFMVGVLPTLNTVIRVKTNKLVCYEDDKL 325
Db 282 T-----LVTATVENETYLTKTNETRQLCFV-----RSKVNIIYC--SDGI 321

Qy 326 WSNWSQEM-----SIGKRNSTLYITMLLIIVPVIIVAGAIIVLLVLYLKLKLIIPPI 380
Db 322 WSESDKQCEGEGDLSKTLRFLWLPF-----GFILILVIVFTGL--LLRKPNTYP 370

Qy 381 GKIFKEMFGD 390
Db 371 -KMIPFFCD 379

RESULT 5
US-11-185-230-2
; Sequence 2, Application US/11/185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 380
; TYPE: PRT 3
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: variant of SEQ ID NO. 2 in which the sequence VRCVTL is substituted
US/11/185,230-12

Query Match      12.7%; Score 293.5; DB 7; Length 378;
Best Local Similarity 27.5%; Pred. No. 1.5e-18;
Matches 94; Conservative 55; Mismatches 130; Indels 63; Gaps 18;

Qy 51 WNPPEGAS--SNCSLWYFSHFQDKQDKKIAPETRISI-----EVLNERICLQVGS 99
Db 53 WQPLSLDHFKECTVEY-----ELKYRNIGSETWTKIITKNLHYKDGFDLKNKIEAKIHT 107

Qy 100 -----QCSNTESEKPSILVEKC--ISPPGDDPESAVTELOCIWHNLSYMKCSWLPGRNTSP 153
Db 108 LLPWQC--TNGSEVQSSWAETTYWIS--PQIGIPETKVQDMDCVYNNWQYLLCSWKPFGIGVLL 165

Qy 154 DTNNTLYYWHRSLEKIHQC--ENIPREGOVFGSPDLTKVKDSSFEQHSVQIMVKDNAGKI 212
Db 166 DTNNTLYYWHRSLEKIHQC--ENIPREGOVFGSPDLTKVKDSSFEQHSVQIMVKDNAGKI 212

Qy 213 KPSEFNIVPLTSRVKPPPHIKNLSFHNH---DLVYQWENPQNF1--SRCLFYEVEVNNST 268
Db 224 RSYFTFQQLQNVKPLPP--VYLTFRESSCEIKLWSIPLGPIPARCFDYEIREDDT 281

Qy 269 ETHNVFYVQEAECNPEFERNVENTS---CFMVGVLPTLNTVIRVKTNKLVCYEDDKL 325
Db 282 T-----LVTATVENETYLTKTNETRQLCFV-----RSKVNIIYC--SDGI 321

Qy 326 WSNWSQEM-----SIGKRNSTLYITMLLIIVPVIIVAGAIIVLLVLYLKLKLIIPPI 380
Db 322 WSESDKQCEGEGDLSKTLRFLWLPF-----GFILILVIVFTGL--LLRKPNTYP 370

Qy 381 GKIFKEMFGD 390
Db 371 -KMIPFFCD 379

US-11-185-230-2
; Sequence 2, Application US/11/185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 380
; TYPE: PRT 3
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: variant of SEQ ID NO. 2 in which the sequence VRCVTL is substituted
US/11-185-230-2

Query Match      12.7%; Score 294.5; DB 7; Length 380;
Best Local Similarity 27.0%; Pred. No. 1.2e-18;
Matches 100; Conservative 59; Mismatches 138; Indels 73; Gaps 20;
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Qy 51 WNPPEGAS--SNCSLWYFSHFQDKQDKKIAPETRISI-----EVLNERICLQVGS 99
Db 53 WQPLSLDHFKECTVEY-----ELKYRNIGSETWTKIITKNLHYKDGFDLKNKIEAKIHT 107

Qy 100 -----QCSNTESEKPSILVEKC--ISPPGDDPESAVTELOCIWHNLSYMKCSWLPGRNTSP 153
Db 108 LLPWQC--TNGSEVQSSWAETTYWIS--PQIGIPETKVQDMDCVYNNWQYLLCSWKPFGIGVLL 165

Qy 154 DTNNTLYYWHRSLEKIHQC--ENIPREGOVFGSPDLTKVKDSSFEQHSVQIMVKDNAGKI 212
Db 166 DTNNTLYYWHRSLEKIHQC--ENIPREGOVFGSPDLTKVKDSSFEQHSVQIMVKDNAGKI 212

Qy 213 KPSEFNIVPLTSRVKPPPHIKNLSFHNH---DLVYQWENPQNF1--SRCLFYEVEVNNST 268
Db 224 RSYFTFQQLQNVKPLPP--VYLTFRESSCEIKLWSIPLGPIPARCFDYEIREDDT 281

Qy 269 ETHNVFYVQEAECNPEFERNVENTS---CFMVGVLPTLNTVIRVKTNKLVCYEDDKL 325
Db 282 T-----LVTATVENETYLTKTNETRQLCFV-----RSKVNIIYC--SDGI 321

Qy 326 WSNWSQEM-----SIGKRNSTLYITMLLIIVPVIIVAGAIIVLLVLYLKLKLIIPPI 380
Db 322 WSESDKQCEGEGDLSKTLRFLWLPF-----GFILILVIVFTGL--LLRKPNTYP 370

Qy 381 GKIFKEMFGD 390
Db 371 -KMIPFFCD 379

RESULT 6
US/11/185
; Sequence 12, Application US/11/185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
; LENGTH: 378
; TYPE: PRT 3
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: variant of SEQ ID NO. 2 in which the sequence VRCVTL is substituted
US/11/185,230-12

Query Match      12.7%; Score 293.5; DB 7; Length 378;
Best Local Similarity 27.5%; Pred. No. 1.5e-18;
Matches 94; Conservative 55; Mismatches 130; Indels 63; Gaps 18;

Qy 51 WNPPEGAS--SNCSLWYFSHFQDKQDKKIAPETRISI-----EVLNERICLQVGS 99
Db 53 WQPLSLDHFKECTVEY-----ELKYRNIGSETWTKIITKNLHYKDGFDLKNKIEAKIHT 107

Qy 100 -----QCSNTESEKPSILVEKC--ISPPGDDPESAVTELOCIWHNLSYMKCSWLPGRNTSP 153
Db 108 LLPWQC--TNGSEVQSSWAETTYWIS--PQIGIPETKVQDMDCVYNNWQYLLCSWKPFGIGVLL 165

Qy 154 DTNNTLYYWHRSLEKIHQC--ENIPREGOVFGSPDLTKVKDSSFEQHSVQIMVKDNAGKI 212
Db 166 DTNNTLYYWHRSLEKIHQC--ENIPREGOVFGSPDLTKVKDSSFEQHSVQIMVKDNAGKI 212

Qy 213 KPSEFNIVPLTSRVKPPPHIKNLSFHNH---DLVYQWENPQNF1--SRCLFYEVEVNNST 268
Db 224 RSYFTFQQLQNVKPLPP--VYLTFRESSCEIKLWSIPLGPIPARCFDYEIREDDT 281

Qy 269 ETHNVFYVQEAECNPEFERNVENTS---CFMVGVLPTLNTVIRVKTNKLVCYEDDKL 325
Db 282 T-----LVTATVENETYLTKTNETRQLCFV-----RSKVNIIYC--SDGI 321

Qy 326 WSNWSQEM-----SIGKRNSTLYITMLLIIVPVIIVAGAIIVLLVLYLKLKLIIPPI 380
Db 322 WSESDKQCEGEGDLSKTLRFLWLPF-----GFILILVIVFTGL--LLRKPNTYP 370

Qy 381 GKIFKEMFGD 390
Db 371 -KMIPFFCD 379
```



```
Qy 308 TVRIRVTKNLCYEDDDKLSNWSQMSIGK 337
      |::| : |::| |::| |::| : |::|
Db 285 DVQRAAVSMCREAG-LWSEWSQPIYVGK 313
      |::| : |::| |::| |::| : |::|

RESULT 9
US-10-511-722-21
; Sequence 21, Application US/10511722
; Publication No. US20050287144A1
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co. Ltd.
; APPLICANT: Wallach, David
; APPLICANT: Shmushkovich, Taisia
; APPLICANT: Ramakrishnan, Parameswaran
; TITLE OF INVENTION: Derivatives of the IL-2 receptor Gamma chain, their preparation a
; FILE REFERENCE: 530
; CURRENT APPLICATION NUMBER: US/10/511,722
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 149217
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 152183
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-722-21

Query Match      8.7%; Score 202; DB 6; Length 341;
Best Local Similarity 27.2%; Pred. No. 1.6e-10;
Matches 72; Conservative 44; Mismatches 101; Indels 48; Gaps 14;

Qy 130 ELQCIWNLNLSYMKCSWLPGRNTSPDNTLYTYWHRSL--EKIHQCN-IFREGQYFGCSF 186
      |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 59 EVQCFVFNVEYMNCTWNSSEPPQ--TNLTLYWYKNSDNKVKQKSHYLFSEITSGC-- 115
      |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

Qy 187 DLTKVKDSSFQHSVQIMVKDNAGKIPSNIVPLTSRVKPDPPHINKLSFH---NDLLY 243
      |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 116 QLOKKEIHLYQTFVVQL--QDPREPRQATQMLKQLNVLVWPAP--ENLTLKLSQLE 171
      |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

Qy 244 WOMENPQNFISRL-----FYEVVNSQTEHNVFYVQEAKEPFEFERNVENTSCFVMP 299
      |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 172 LNWNN--RFLNHCLEHLVQYRTDWDHWT-----EQSDYRHKFSLP 211
      |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

Qy 300 GVLPTLNTVIRVTKNLCYEDDDKLSNWSQMSIG---KKNSTLYITMLLIVPVIVA 356
      |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 212 SVDGQKRYTFRVRSRFPNPLC-GSAQHWSSEWHPHIGSNTSKENPFLFALEAVVISVGS 270
      |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

Qy 357 GAIIVLL---LYLKRKLKIIIPPIP 378
      |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 271 GLIISLLCVYFWLER-----TMPRIIP 291
      |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

RESULT 11
US-11-105-268-60
; Sequence 60, Application US/11105268
; Publication No. US20050260204A1
; GENERAL INFORMATION:
; APPLICANT: Allan, Christian
; TITLE OF INVENTION: ANTI-IL-9 ANTIBODY FORMULATIONS AND USES THEREOF
; FILE REFERENCE: 10271-126-999
; CURRENT APPLICATION NUMBER: US/11/105,268
; CURRENT FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: 60/561,845
; PRIOR FILING DATE: 2004-04-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-268-60

Query Match      8.7%; Score 202; DB 7; Length 369;
Best Local Similarity 27.2%; Pred. No. 1.8e-10;
Matches 72; Conservative 44; Mismatches 101; Indels 48; Gaps 14;

Qy 130 ELQCIWNLNLSYMKCSWLPGRNTSPDNTLYTYWHRSL--EKIHQCN-IFREGQYFGCSF 186
      |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 59 EVQCFVFNVEYMNCTWNSSEPPQ--TNLTLYWYKNSDNKVKQKSHYLFSEITSGC-- 115
      |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

Qy 187 DLTKVKDSSFQHSVQIMVKDNAGKIPSNIVPLTSRVKPDPPHINKLSFH---NDLLY 243
      |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 116 QLOKKEIHLYQTFVVQL--QDPREPRQATQMLKQLNVLVWPAP--ENLTLKLSQLE 171
      |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

Qy 244 WOMENPQNFISRL-----FYEVVNSQTEHNVFYVQEAKEPFEFERNVENTSCFVMP 299
      |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 172 LNWNN--RFLNHCLEHLVQYRTDWDHWT-----EQSDYRHKFSLP 211
      |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

Qy 300 GVLPTLNTVIRVTKNLCYEDDDKLSNWSQMSIG---KKNSTLYITMLLIVPVIVA 356
      |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 212 SVDGQKRYTFRVRSRFPNPLC-GSAQHWSSEWHPHIGSNTSKENPFLFALEAVVISVGS 270
      |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

Qy 357 GAIIVLL---LYLKRKLKIIIPPIP 378
      |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 271 GLIISLLCVYFWLER-----TMPRIIP 291
      |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

RESULT 10
US-10-511-722-20
; Sequence 20, Application US/10511722
; Publication No. US20050287144A1
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co. Ltd.
; APPLICANT: Wallach, David
; APPLICANT: Shmushkovich, Taisia
; APPLICANT: Ramakrishnan, Parameswaran
; TITLE OF INVENTION: Derivatives of the IL-2 receptor Gamma chain, their preparation a
; FILE REFERENCE: 530
; CURRENT APPLICATION NUMBER: US/10/511,722
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 149217
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 152183
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 21
```


INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-636-320-2

Query Match 7.5%; Score 173; DB 6; Length 708;
Best Local Similarity 25.0%; Pred. No. 1.5e-07;
Matches 101; Conservative 51; Mismatches 194; Indels 58; Gaps 21;
QY 31 QPVTNLSVSNELCTVIWTPPPGASSNCSLWYFHFHG-DKQDKKIAPETRRSIEVPL 89
DB 34 ESPVQLHSNFTAVCVLKEKCMDFHVNANIVWKNHFTIPKEQYTIINRTASSVTFTD 93
QY 90 NERICLOVGSQCSTNESEKPSILVEKCIS--PPEGDPESAVTELQCIWHNLSYMKCSWLP 147
DB 94 IASLNIQLTCNLTGQLEQNVYGITIISGLPPE-KPKN----LSCI VNEGKKWRCWDG 148
QY 148 GRNTSPDNTYTL-YYWHRSLKIHOCENIFREGQYFGCSFDLTKVKDSSPEQHSVQIMVK 206
DB 149 GRETHLETNFTLKSEW--ATHKPADCK--AKRDTPTCTVDYSTV---YFVNIEVWVEAE 201
QY 207 DNAGKI-KPSFNIVPLTSRVKPPPHIKNLSFHND-----LYQWENPQNFISRCIFYE 260
DB 202 NALGKVTSDHINFDPV-YKVKPNPPH--NLSVINSEBELSSILKLTWNTNPSIKSVIILKYN 258
QY 261 VEVNNSQTETHNVFVQAEKCNPEPERNVENTSCFMVPGVLPDTLNTVIRVKTNKLKY 320
DB 259 IQYRTKDASTWS-----QIPP-EDTASTRSSFTVQDLKPFTEYVFRIR-----CM 302
QY 321 EDD--KLMSNWSQEMS--IGKRNSTLYITMLLIVPVIVAGAIIVLLLYLKLKLIIPPP 376
DB 303 KEDGKGWSDWSERASGITVEDRPSKAPSPWKIDPSHTQGYRTVQLVW-KTL-----PP 356
QY 377 IPDPGKIPKEMFGDNDTLHWKYDIYEKQTKETDSVVLLEN 420
DB 357 FEANGKIL-----DYEVTLTRWESH--LQNYTVNATKLTVNLTN 393

RESULT 15

US-10-995-561-696
; Sequence 696, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 696
; LENGTH: 918
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-696

Query Match 7.5%; Score 173; DB 6; Length 918;
Best Local Similarity 25.0%; Pred. No. 2e-07;
Matches 101; Conservative 51; Mismatches 194; Indels 58; Gaps 21;

QY 31 QPVTNLSVSNELCTVIWTPPPGASSNCSLWYFHFHG-DKQDKKIAPETRRSIEVPL 89
DB 34 ESPVQLHSNFTAVCVLKEKCMDFHVNANIVWKNHFTIPKEQYTIINRTASSVTFTD 93
QY 90 NERICLOVGSQCSTNESEKPSILVEKCIS--PPEGDPESAVTELQCIWHNLSYMKCSWLP 147
DB 94 IASLNIQLTCNLTGQLEQNVYGITIISGLPPE-KPKN----LSCI VNEGKKWRCWDG 148

QY 148 GRNTSPDNTYTL-YYWHRSLKIHOCENIFREGQYFGCSFDLTKVKDSSPEQHSVQIMVK 206
DB 149 GRETHLETNFTLKSEW--ATHKPADCK--AKRDTPTCTVDYSTV---YFVNIEVWVEAE 201
QY 207 DNAGKI-KPSFNIVPLTSRVKPPPHIKNLSFHND-----LYQWENPQNFISRCIFYE 260
DB 202 NALGKVTSDHINFDPV-YKVKPNPPH--NLSVINSEBELSSILKLTWNTNPSIKSVIILKYN 258
QY 261 VEVNNSQTETHNVFVQAEKCNPEPERNVENTSCFMVPGVLPDTLNTVIRVKTNKLKY 320
DB 259 IQYRTKDASTWS-----QIPP-EDTASTRSSFTVQDLKPFTEYVFRIR-----CM 302
QY 321 EDD--KLMSNWSQEMS--IGKRNSTLYITMLLIVPVIVAGAIIVLLLYLKLKLIIPPP 376
DB 303 KEDGKGWSDWSERASGITVEDRPSKAPSPWKIDPSHTQGYRTVQLVW-KTL-----PP 356
QY 377 IPDPGKIPKEMFGDNDTLHWKYDIYEKQTKETDSVVLLEN 420
DB 357 FEANGKIL-----DYEVTLTRWESH--LQNYTVNATKLTVNLTN 393

Search completed: February 8, 2006, 22:35:22
Job time : 10.2851 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 21:52:58 ; Search time 98.483 Seconds
(without alignments)
1427.670 Million cell updates/sec

Title: US-10-036-568A-4_COPY_26_345
Perfect score: 1760
Sequence: 1 APTQTQPVNLSVSNELC.....WSNWSQEMSGCKKSTLYI 320

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: geneseqp1980a.*
2: geneseqp1990a.*
3: geneseqp2000a.*
4: geneseqp2001a.*
5: geneseqp2002a.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1760	100.0	414	8	Adx97531 Pancreati
2	1760	100.0	426	2	Aaw09822 Human int
3	1760	100.0	427	2	Aaw24973 Human int
4	1760	100.0	427	4	Aabi19807 Human int
5	1760	100.0	427	7	Adf17835 Human IL-
6	1760	100.0	427	8	Adl171812 Human int
7	1760	100.0	427	8	Adl171814 Human int
8	1760	100.0	427	8	Adl82843 Human PRO
9	1760	100.0	427	8	Adn04504 Antipsori
10	1760	100.0	427	8	Adn62575 Human int
11	1760	100.0	427	8	Abm82441 Tumour-as
12	1754	99.7	427	4	Aabi19808 Human int
13	1754	99.7	427	8	Adl171813 Human int
14	1745	99.1	322	5	Aae13745 Human sol
15	1745	99.1	664	7	Adf17841 Chimeric
16	1745	99.1	784	3	Aay92207 IL-13/IL-
17	1745	99.1	784	7	Abw02180 Human IL-
18	1745	99.1	793	3	Aay92208 IL-13/IL-
19	1745	99.1	793	7	Abw02181 Human IL-
20	1478	84.0	405	4	Aaw09132 Canine in
21	1324	75.2	426	2	Aaw09821 Mouse int
22	1314	74.7	424	9	Adx97888 Murine IL
23	1124	63.9	286	4	Aab90678 Human DAL
24	773	43.9	177	2	Aaw58987 Homo sapi

25	296	16.8	318	4	AAU69137	Aau69137 Canine IL
26	296	16.8	365	4	AAU69136	Aau69136 Canine in
27	296	16.8	386	4	AAU69135	Aau69135 Canine in
28	296	16.8	561	4	AAU69138	Aau69138 Canine IL
29	296	16.8	561	4	AAU69141	Aau69141 Canine IL
30	296	16.8	563	4	AAU69140	Aau69140 Canine IL
31	296	16.8	565	4	AAU69139	Aau69139 Canine IL
32	289	16.4	372	2	AAW36616	Aaw36616 Celebus m
33	287	16.3	82	8	ADO26844	Ado26844 Human rec
34	284	16.1	310	8	ADO75553	Ado75553 IL13-R-al
35	284	16.1	315	2	AAW56261	Aaw56261 Mature in
36	284	16.1	317	5	AAE13746	Aae13746 Human sol
37	284	16.1	359	2	AAW56260	Aaw56260 Construct
38	284	16.1	380	2	AAW36613	Aaw36613 Human Zcy
39	284	16.1	380	2	AAW35295	Aaw35295 Human IL-
40	284	16.1	380	2	AAW24972	Aaw24972 Human int
41	284	16.1	380	2	AAW33603	Aaw33603 Homo sapi
42	284	16.1	380	2	AAW41502	Aaw41502 Human cyt
43	284	16.1	380	2	AAW41520	Aaw41520 Human HR-
44	284	16.1	380	3	RAY95296	Aay95296 IL-13 bin
45	284	16.1	380	4	AAG63812	Aag63812 Amino aci

ALIGNMENTS

RESULT 1
ADX97531
ID ADX97531 standard; protein; 414 AA.
XX
AC ADX97531;
XX
DT 21-APR-2005 (first entry)
XX
DE Pancreatic cancer associated human protein, SEQ ID 79.
XX
KW pancreas tumor; cytostatic.
XX
OS Homo sapiens.
XX
PN EPI471075-A2.
XX
PD 27-OCT-2004.
XX
PF 31-MAR-2004; 2004EP-00090124.
XX
PR 31-MAR-2003; 2003DE-01015834.

(HINZ/) HINZMANN B.
(ROSE/) ROSENTHAL A.
(PILA/) PILARSKY C.
(DAHL/) DAHL E.
(SPEC/) SPECHT T.
(LICH/) LICHTNER R.
Rosenthal A, Pilarisky C, Dahl E, Specht T, Bruemendorf T;
Lichtner R, Staub E, Roepcke S, Li X;
WPI; 2004-768082/76.
N-PSDB; ADX97460.

New nucleic acid differentially expressed in pancreatic tumor tissue, for use as diagnostic agents and in screening for therapeutic agents.

Claim 2; SEQ ID NO 79; 28pp; German.

The invention relates to a novel human nucleic acid sequence of the pancreas and its encoded protein. The invention further comprises: proteins and peptides, preferably isolated, that contain a sequence encoded by the novel nucleic acid; and methods for diagnosis and treatment of pancreatic cancer, using a substance that inhibits or binds to the protein or its DNA, including: an antisense oligonucleotide, short interfering RNA or ribozyme directed against the pancreatic protein, an

Db	326	WSNWSQEMSIGKRNSTLYI 345	
AAW24973			
AAW24973		standard; protein; 427 AA.	
AAW24973			
22-JUN-1998		(first entry)	
Human interleukin-13		alpha receptor.	
Interleukin-13		receptor; diagnosis; inflammation; allergy; IL-13.	
Homo sapiens.			
WO9720926-A1.			
12-JUN-1997.			
07-NOV-1996;		96WO-FR001756.	
06-DEC-1995;		95FR-00014424.	
(SNFI) SANOFI SA.			
Caput D, Ferrara P, Laurent P, Vita N;			
WPI; 1997-319773/29.			
N-PSDB; AAT85827.			
New purified human interleukin-13		receptors - and related nucleic acids,	
useful for diagnosis and treatment of inflammation, allergy, etc.			
Claim 8; Page 46-47; 83pp; French.			
This sequence represents interleukin-13		(IL-13) alpha receptor. The	
invention relates to new purified peptides		comprising 380 or 427 amino	
acid sequences, which are receptors for		interleukin-13 (IL-13); the 380	
and 427 aa proteins are designated		IL-13R beta and alpha respectively.	
The IL-13R beta has high affinity for		IL-13 while IL-13R alpha has low	
affinity, but acquires high affinity		when associated with the IL-4	
receptor. Nucleic acids encoding		IL-13R beta and alpha are used as	
diagnostic probes to identify aberrant		synthesis or genetic anomalies	
such as loss of heterozygosity and		rearrangements, or chromosomal	
anomalies. They are also used for		production of recombinant IL-13R	
and alpha which can be used as		IL-13 antagonists, specifically to	
regulate IL-13-induced responses		for treatment of inflammation and	
allergy. IL-13 receptors are also		useful as antisense molecules for	
therapy (blocking synthesis of		IL-13R). Antibodies are used (in	
immunoassays) to diagnose diseases		associated with abnormal expression	
of IL-13 receptors; when coupled to		a toxin also for treatment of	
overproduction of IL-13R. Cells		that express IL-13R at the surface	
used to identify ligands and		modulators of IL-13R	
Sequence 427 AA;			
Query Match	100.0%;	Score 1760; DB 2; Length 427;	
Best Local Similarity	100.0%;	Pred. No. 4.1e-164;	
Matches 320; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;	
1	APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNC	SLMYFSGHFGDKDKKIAPETRRSI 60	
27	APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNC	SLMYFSGHFGDKDKKIAPETRRSI 86	
61	EYPLNERICLVGSCQSTNESKPSILVEKCI	SPPEGDPESAVTELQCIWHNLSYMKCSW 120	
87	EYPLNERICLVGSCQSTNESKPSILVEKCI	SPPEGDPESAVTELQCIWHNLSYMKCSW 146	
121	LPGRNTSPDNTYTLYYWHSLEKIHOCENI	FREGQYFGCSFDLTKVKDSSFEQHSVQIMV 180	
147	LPGRNTSPDNTYTLYYWHSLEKIHOCENI	FREGQYFGCSFDLTKVKDSSFEQHSVQIMV 206	
Qy	181	KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHND	LYVQWENPQNFISRCLFYEVVNN 240
Db	207	KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHND	LYVQWENPQNFISRCLFYEVVNN 266
Qy	241	SQTETHNVFVQEAACENPFRNVENTSCFMVPGVL	PDTLNTVYIRVKTNKLCEYEDDKL 300
Db	267	SQTETHNVFVQEAACENPFRNVENTSCFMVPGVL	PDTLNTVYIRVKTNKLCEYEDDKL 326
Qy	301	WSNWSQEMSIGKRNSTLYI 320	
Db	327	WSNWSQEMSIGKRNSTLYI 346	
RESULT 4			
AAI19807			
ID	AAI19807	standard; protein; 427 AA.	
XX	AAI19807;		
XX	05-MAR-2001	(first entry)	
XX	Human interleukin-13	receptor alpha-1.	
XX	Interleukin-13	receptor alpha-1; interleukin-4; human; atopy;	
XX	atopic dermatitis; allergy; rhinitis; eczema;	AIDS;	
XX	dermatological; antiasthmatic; antiallergic;	therapy; diagnosis.	
XX	Homo sapiens.		
Key	Location/Qualifiers		
FT	Peptide	1..26	
FT	Domain	/label= Sig_peptide	
FT	Protein	27..347	
FT	Protein	/label= Extracellular_domain	
FT	Protein	28..427	
FT	Protein	/label= Mature_protein	
FT	Protein	327..331	
FT	Protein	/note= "WSXWS motif conserved in the type-I cytokine	
FT	Protein	receptor superfamily"	
FT	Protein	348..367	
FT	Protein	/label= Transmembrane_domain	
FT	Protein	368..427	
FT	Protein	/label= Cytoplasmic_domain	
FT	Protein	405..408	
FT	Protein	/note= "YXXQ motif, consensus for STAT binding"	
FT	Protein	US6143871-A.	
FT	Protein	07-NOV-2000.	
FT	Protein	12-NOV-1997; 97US-00969125.	
FT	Protein	13-DEC-1996; 96GB-00025899.	
FT	Protein	(GAUC/) GAUCHAT J.	
FT	Protein	(BONN/) BONNEFOY J.	
FT	Protein	Gauchat J, Bonnefoy J;	
FT	Protein	WPI; 2001-006445/01.	
FT	Protein	N-PSDB; AAA88907.	
FT	Protein	Novel polypeptide capable of binding interleukin-13 or interleukin-4	
FT	Protein	useful for treating atopy, atopic dermatitis, allergies, rhinitis,	
FT	Protein	eczema, asthma or AIDS.	
FT	Protein	Claim 2; Fig 1A; 26pp; English.	
FT	Protein	The present sequence is that of a protein capable of binding human	
FT	Protein	interleukin-13 (IL-13) and/or human interleukin-4 (IL-4) in the presence	
FT	Protein	of IL-4 receptor alpha. It was deduced from cDNA (see AAA88907) isolated	
FT	Protein	from a human activated tonsillar cDNA library. This IL-13 receptor alpha-1	

CC polypeptide can be used to inhibit IL-13 or IL-4 induced IgE synthesis in
CC B cells, useful in the treatment of diseases in which IgE or Th2
CC differentiation plays a role, e.g. atopy, atopic dermatitis, allergy,
CC rhinitis, eczema, asthma or AIDS. Antibodies raised against the
CC polypeptide are useful for detecting IL-13 and IL-4 receptor or parts of
CC them which have been shed from cells as a result of disease, e.g. cancer,
CC leukaemia, atopy, atopic dermatitis, allergies, rhinitis, eczema, asthma,
CC lupus erythematosus, AIDS, thyroiditis, diabetes, uveitis, dermatitis,
CC psoriasis, urticaria, nephrotic syndrome, inflammatory bowel disease,
CC glomerulonephritis, ulcerative colitis, Crohn's disease, Sjogren's
CC syndrome and toxoplasmosis
XX
SQ Sequence 427 AA;

Query Match 100.0%; Score 1760; DB 4; Length 427;
Best Local Similarity 100.0%; Pred. No. 4.1e-164;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APTETQPPVNLVSVENLCTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 60
DB 27 APTETQPPVNLVSVENLCTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 86
QY 61 EVPLNERICLVGSCSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNL SYMKCSW 120
DB 87 EVPLNERICLVGSCSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNL SYMKCSW 146
QY 121 LPGRNTSPDNTYLYYWHRSLEKIHQCNIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
DB 147 LPGRNTSPDNTYLYYWHRSLEKIHQCNIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 206
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYQWENPQNFISRCIFYEVEVNN 240
DB 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYQWENPQNFISRCIFYEVEVNN 266
QY 241 SQTETHNVFYQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKL CYEDDKL 300
DB 267 SQTETHNVFYQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKL CYEDDKL 326
QY 301 WSNWSQEMSIGKKRNSTLYI 320
DB 327 WSNWSQEMSIGKKRNSTLYI 346

RESULT 5
ADFI7835
ID ADFI7835 standard; protein; 427 AA.
XX
AC ADFI7835;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human IL-13 alpha 1 receptor (IL-13R) protein.
XX
KW IL-13R; human; receptor; anaphylaxis; hay fever; asthma;
KW antiinflammatory; cytostatic; antiulcer; dermatological; antiallergic;
KW antisthmatic; fibrosis; Hodgkin's disease; ulcerative colitis;
KW scleroderma; allergic rhinitis; oncological;
KW chronic obstructive pulmonary disease.
XX
OS Homo sapiens.
XX
PN WO2003080675-A2.
XX
PD 02-OCT-2003.
XX
PF 21-MAR-2003; 2003WO-AU000352.
XX
PR 22-MAR-2002; 2002AU-00001301.
PR 03-FEB-2003; 2003AU-00900437.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Dunlop FM, Baca M, Nash AD, Fabri LJ;

XX
DR WPI; 2003-876912/81.
XX N-PSDB; ADFI7834.
PT New monoclonal antibodies against interleukin-13 receptor alpha, useful
PT for treating fibrosis, Hodgkin's disease, ulcerative colitis,
PT scleroderma, allergic rhinitis, oncological conditions, asthma or an
PT inflammatory disorder.
XX
PS Disclosure; SEQ ID NO 4; 99pp; English.
XX

This invention relates to a novel antibodies that function as interleukin
-13 receptor alpha-1 chain (IL-13R alpha-1) antagonists and can be used
for treating certain conditions induced by IL-13. Specifically, it refers
to antibodies that bind to IL-13R alpha-1 and inhibit or modulate IL-13
and IL-4 induced signalling. IL-13 is a mediator in the immunostimulatory
system, such that it is involved in the induction of IgE, IgG4 and T-
helper cells and accordingly is implicated in conditions from anaphylaxis
to hay fever and asthma. As such, the present invention describes these
novel antibodies as antiinflammatory, cytostatic, antiulcer, and
dermatological, antiallergic and antisthmatic. The methods and
compositions are useful for treating various disorders including
fibrosis, Hodgkin's disease, ulcerative colitis, scleroderma, allergic
rhinitis, oncological conditions and chronic obstructive pulmonary
disease. This polypeptide sequence is the human IL-13 alpha 1 receptor
protein of the invention.

XX
SQ Sequence 427 AA;

Query Match 100.0%; Score 1760; DB 7; Length 427;
Best Local Similarity 100.0%; Pred. No. 4.1e-164;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APTETQPPVNLVSVENLCTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 60
DB 27 APTETQPPVNLVSVENLCTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 86
QY 61 EVPLNERICLVGSCSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNL SYMKCSW 120
DB 87 EVPLNERICLVGSCSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNL SYMKCSW 146
QY 121 LPGRNTSPDNTYLYYWHRSLEKIHQCNIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
DB 147 LPGRNTSPDNTYLYYWHRSLEKIHQCNIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 206
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYQWENPQNFISRCIFYEVEVNN 240
DB 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYQWENPQNFISRCIFYEVEVNN 266
QY 241 SQTETHNVFYQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKL CYEDDKL 300
DB 267 SQTETHNVFYQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKL CYEDDKL 326
QY 301 WSNWSQEMSIGKKRNSTLYI 320
DB 327 WSNWSQEMSIGKKRNSTLYI 346

RESULT 6
ADFI7812
ID ADFI7812 standard; protein; 427 AA.
XX
AC ADFI7812;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human interleukin-13 receptor alpha (IL-13 Ralpha) protein.
XX
KW Human; IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis;
KW eczema; asthma; AIDS; gene therapy; interleukin; receptor.
XX
OS Homo sapiens.
XX

PH Key Location/Qualifiers
FT Peptide 1..26
FT Protein /label= Signal_peptide
FT Domain 27..427
FT Domain /note= "Human mature IL-13 R protein"
FT Domain 27..347
FT Domain /note = Extracellular domain
FT Domain 327..331
FT Domain /note = WSXWS motif
FT Domain 368..427
FT Domain /note = Cytoplasmic domain
XX US2004043921-A1.
XX 04-MAR-2004.
XX 29-SEP-2003; 2003US-00671697.
XX 13-DEC-1996; 96GB-00025899.
XX 12-NOV-1997; 97US-00969125.
XX 06-APR-2000; 2000US-00545002.
XX (BONN/) BONNEFOY J.
XX (GAUC/) GAUCHAT J.
XX Bonnefoy J, Gauchat J;
XX WPI; 2004-225726/21.
XX N-PSDB; ADL71811.
XX Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse
XX effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma
XX or AIDS, comprises administering a polypeptide or soluble polypeptide.
XX Claim 1; SEQ ID NO 9; 27pp; English.
XX The invention relates to polypeptides capable of binding human
XX interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpha. The
XX invention also relates to a method of treatment of a disease in which
XX IL13 and IL4 cause adverse effects. The method is useful for treating a
XX disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic
XX dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides
XX of the invention are useful in raising antibodies. It is also useful in
XX gene therapy. The present sequence is human interleukin-13 receptor alpha
XX (IL-13 Ralpha) protein.
XX Sequence 427 AA;
XX Query Match 100.0%; Score 1760; DB 8; Length 427;
XX Best Local Similarity 100.0%; Pred. No. 4.1e-164;
XX Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APTETQPPVTNLSVSVENLCTVIWTPNPEGASSNCSLWYFSHFGDKQDKKIAPETRRSI 60
DB 27 APTETQPPVTNLSVSVENLCTVIWTPNPEGASSNCSLWYFSHFGDKQDKKIAPETRRSI 86
QY 61 EYPLNERICLQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120
DB 87 EYPLNERICLQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 146
QY 121 LPRGNTSPDNTYLYWHRSLKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
DB 147 LPRGNTSPDNTYLYWHRSLKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 206
QY 181 KDNAGKIKPSNIVPLTSRKVPDPPIKNSLPHNDLLVQWENPNQFTSRCLFYEVEVNN 240
DB 207 KDNAGKIKPSNIVPLTSRKVPDPPIKNSLPHNDLLVQWENPNQFTSRCLFYEVEVNN 266
QY 241 SQTETHNIFYVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYDDKL 300
DB 267 SQTETHNIFYVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYDDKL 326
QY 301 WSNWSQEMSIGKKRNSTLYI 320

Db 327 WSNWSQEMSIGKKRNSTLYI 346
RESULT 7
ADL71814
ID ADL71814 standard; protein; 427 AA.
XX AC ADL71814;
XX 20-MAY-2004 (first entry)
XX Human interleukin-13 receptor alpha (IL-13 Ralpha) mutant, G358D.
XX Human; IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis;
XX eczema; asthma; AIDS; gene therapy; interleukin; receptor; mutant;
XX mutein.
XX Homo sapiens.
XX Synthetic.
XX Key Location/Qualifiers
FT Misc-difference 358 /note= "Wild-type Gly is substituted with Asp"
FT US2004043921-A1.
XX 04-MAR-2004.
XX 29-SEP-2003; 2003US-00671697.
XX 13-DEC-1996; 96GB-00025899.
XX 12-NOV-1997; 97US-00969125.
XX 06-APR-2000; 2000US-00545002.
XX (BONN/) BONNEFOY J.
XX (GAUC/) GAUCHAT J.
XX Bonnefoy J, Gauchat J;
XX WPI; 2004-225726/21.
XX Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse
XX effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma
XX or AIDS, comprises administering a polypeptide or soluble polypeptide.
XX Claim 14; Page; 27pp; English.
XX The invention relates to polypeptides capable of binding human
XX interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpha. The
XX invention also relates to a method of treatment of a disease in which
XX IL13 and IL4 cause adverse effects. The method is useful for treating a
XX disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic
XX dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides
XX of the invention are useful in raising antibodies. It is also useful in
XX gene therapy. The present sequence is human interleukin-13 receptor alpha
XX (IL-13 Ralpha) mutant protein. Note: This sequence is not shown in the
XX specification, however it is constructed based on human IL-13 Ralpha
XX protein shown as SEQ ID NO:9 in the specification.
XX Sequence 427 AA;
XX Query Match 100.0%; Score 1760; DB 8; Length 427;
XX Best Local Similarity 100.0%; Pred. No. 4.1e-164;
XX Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APTETQPPVTNLSVSVENLCTVIWTPNPEGASSNCSLWYFSHFGDKQDKKIAPETRRSI 60
DB 27 APTETQPPVTNLSVSVENLCTVIWTPNPEGASSNCSLWYFSHFGDKQDKKIAPETRRSI 86
QY 61 EYPLNERICLQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120
DB 87 EYPLNERICLQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 146

QY 121 LPRGNTSPDNTYTLYYMHSLEKIHQENIFREGQYFGCSFDLTWKDSSFQHSQIIMV 180
Db 147 LPRGNTSPDNTYTLYYMHSLEKIHQENIFREGQYFGCSFDLTWKDSSFQHSQIIMV 206
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNFISRCLFYEVVNN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNFISRCLFYEVVNN 266
QY 241 SQTETHNVFVQBAKCNPEFRNVENTSCFMVPGVLPDTLNTVRIRVTKNKL CYEDDKL 300
Db 267 SQTETHNVFVQBAKCNPEFRNVENTSCFMVPGVLPDTLNTVRIRVTKNKL CYEDDKL 326
QY 301 WSNWSQEMSIGKRNSTLYI 320
Db 327 WSNWSQEMSIGKRNSTLYI 346
RESULT 8
ADL82843
ID ADL82843 standard; protein; 427 AA.
XX AC ADL82843;
XX XX
XX 17-JUN-2004 (first entry)
XX XX
XX Human PRO2537, SEQ ID 45.
XX XX
XX Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
KW Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
KW Gene Therapy; PRO: B cell related disorder; cancer;
KW immune-mediated inflammatory disease; human.
XX XX
OS Homo sapiens.
XX XX
XX WO2004024097-A2.
XX PD 25-MAR-2004.
XX XX
XX 15-SEP-2003; 2003WO-US029097.
PF XX
XX 16-SEP-2002; 2002US-0411392P.
PR XX
XX (GETH) GENENTECH INC.
PA Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
PI Wu TD;
XX XX
XX WPI: 2004-329389/30.
DR N-PSDB; ADL82842.
XX XX
XX New PRO polypeptide, useful for diagnosing and treating a B cell related
PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
XX PS
XX Claim 10; Fig 45; 695pp; English.
XX XX
XX The present invention relates to PRO proteins and their coding sequences.
CC The PRO proteins are useful for diagnosing and treating a B cell related
CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide
CC antigen unresponsiveness, selective IgA deficiency, selective IgM
CC deficiency, selective deficiency of IgG subclasses, immunodeficiency with
CC hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's
CC lymphoma, intermediate lymphoma, follicular lymphoma, type II
CC hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic
CC anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
CC ankylosing spondylitis. The PRO proteins are also useful for preparing a
CC medicament for treating a condition that is responsive to the PRO
CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
CC coding sequences are useful as hybridization probes in chromosome and
CC gene mapping, in preparing PRO proteins, or in generating transgenic
CC animals or knockout animals, which in turn are useful in the development
CC and screening of therapeutically useful reagents.

XX SQ Sequence 427 AA;
Query Match 100.0%; Score 1760; DB 8; Length 427;
Best Local Similarity 100.0%; Pred. No. 4.1e-164;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APETETOPPTNLSVSVENICTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 60
Db 27 APETETOPPTNLSVSVENICTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 86
QY 61 EYPLNERICLOVGSQCSTNESEKPSILVEKICISPPGDPESA VTELCQCIWHNLSYMKCSW 120
Db 87 EYPLNERICLOVGSQCSTNESEKPSILVEKICISPPGDPESA VTELCQCIWHNLSYMKCSW 146
QY 121 LPRGNTSPDNTYTLYYMHSLEKIHQENIFREGQYFGCSFDLTWKDSSFQHSQIIMV 180
Db 147 LPRGNTSPDNTYTLYYMHSLEKIHQENIFREGQYFGCSFDLTWKDSSFQHSQIIMV 206
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNFISRCLFYEVVNN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNFISRCLFYEVVNN 266
QY 241 SQTETHNVFVQBAKCNPEFRNVENTSCFMVPGVLPDTLNTVRIRVTKNKL CYEDDKL 300
Db 267 SQTETHNVFVQBAKCNPEFRNVENTSCFMVPGVLPDTLNTVRIRVTKNKL CYEDDKL 326
QY 301 WSNWSQEMSIGKRNSTLYI 320
Db 327 WSNWSQEMSIGKRNSTLYI 346
RESULT 9
ADN04504
ID ADN04504 standard; protein; 427 AA.
XX AC ADN04504;
XX XX
XX 01-JUL-2004 (first entry)
DT XX
XX Antipsoriatic protein sequence #445.
DE XX
XX antipsoriatic; gene therapy; psoriasis; diagnosis.
KW
XX Homo sapiens.
OS
XX WO2004028479-A2.
PN XX
XX 08-APR-2004.
PD XX
XX 25-SEP-2003; 2003WO-US030907.
PF XX
XX 25-SEP-2002; 2002US-0414006P.
PR XX
XX (GETH) GENENTECH INC.
PA Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI Wu TD;
XX XX
XX WPI: 2004-305105/28.
DR N-PSDB; ADN04503.
XX XX
XX New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.
XX PS
XX Claim 9; SEQ ID NO 898; 3069pp; English.
XX XX
XX The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polypeptides of the invention.

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XX SQ Sequence 427 AA;
Query Match 100.0%; Score 1760; DB 8; Length 427;
Best Local Similarity 100.0%; Pred. No. 4.1e-164;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRISI 60
DB 27 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRISI 86
QY 61 EVPLNERICLQVGSQCSTNESEKPSILVEKICISPEGDPESAVTELOCIWHNLSYMKCSW 120
DB 87 EVPLNERICLQVGSQCSTNESEKPSILVEKICISPEGDPESAVTELOCIWHNLSYMKCSW 146
QY 121 LPGRTSPDNTYLYWHRSLKIHQCEINIFREQYFGCSPDLTKVKDSSFEQHSVQIMV 180
DB 147 LPGRTSPDNTYLYWHRSLKIHQCEINIFREQYFGCSPDLTKVKDSSFEQHSVQIMV 206
QY 181 KDNAGKIKPSFNIVPLTSRVKPDPPHKNLSFHNDLLVQWENPQNFISRCCLFYEVVNN 240
DB 207 KDNAGKIKPSFNIVPLTSRVKPDPPHKNLSFHNDLLVQWENPQNFISRCCLFYEVVNN 266
QY 241 SOTETHNVFVQAEKACENPERNVNTSCPMVPGVLPDNTLTNTRIRVKTNKLCEYDDKL 300
DB 267 SOTETHNVFVQAEKACENPERNVNTSCPMVPGVLPDNTLTNTRIRVKTNKLCEYDDKL 326
QY 301 WSNWSQEMSIGKKRNSTLYI 320
DB 327 WSNWSQEMSIGKKRNSTLYI 346

RESULT 10
ADN62575
ID ADN62575 standard; protein; 427 AA.
XX AC ADN62575;
XX 12-AUG-2004 (first entry)
XX Human interleukin 13 (IL-13) receptor alpha 1 chain.
XX Human; receptor; cytokine; interleukin 13 receptor alpha 1 chain; IL-13;
XX IL-4; atopy; atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;
XX cancer; inflammatory disease; rheumatoid arthritis;
XX inflammatory bowel disease; multiple sclerosis; Alzheimer's disease;
XX Lupus erythematosus; thyroiditis; diabetes; uveitis; psoriasis;
XX urticaria; nephrotic syndrome; glomerulonephritis; ulcerative colitis;
XX Crohn's disease; Sjogren's syndrome; toxoplasmosis; listeriosis; leprosy;
XX Lyme disease; tuberculosis; malaria; leishmaniasis.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX Peptide 1..26
XX FT /note= "Signal peptide"
XX FT Protein 27..427
XX FT /note= "Mature protein claimed in claim 1"
XX FT
XX US6743604-B1.
XX 01-JUN-2004.
XX 06-APR-2000; 2000US-00545002.
XX 13-DEC-1996; 96GB-00025899.
XX 12-NOV-1997; 97US-00969125.
XX (SMK ) SMITHKLINE BEECHAM CORP.
XX PA
XX Bonnefoy J, Gauchat J;
XX WPI; 2004-409324/38.
XX DR
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DR N-PSDB; ADN62574.
XX New isolated nucleic acid molecule encoding a polypeptide capable of
XX binding human IL-13 and/or binding human IL-4, useful in medicine, in
XX diagnostics or for producing antibodies.
XX Claim 1; SEQ ID NO 9; 24pp; English.
XX The invention relates to an isolated nucleic acid molecule (ADN62574),
XX which encodes the mature form of a polypeptide capable of binding human
XX IL-13 (interleukin 13, a cytokine) and/or binding human IL-4 (designated
XX IL-13 receptor alpha 1 subunit) appearing as ADN62575. Also included are
XX a vector comprising the nucleic acid molecule and a host cell comprising
XX the vector. The nucleic acids are useful as probes or primers or in the
XX analysis of allelic variation. The polypeptides are useful for binding
XX human IL-13 and/or binding human IL-4 and act as inhibitors by
XX interfering with the interaction between human IL-13 or IL-4 and their
XX natural receptors. They can also be used in medicine, e.g. for treatment
XX of diseases such as atopy, atopic dermatitis, allergy, rhinitis, eczema,
XX asthma, AIDS, cancer, inflammatory disease (e.g. rheumatoid arthritis and
XX inflammatory bowel disease), multiple sclerosis, Alzheimer's disease,
XX Lupus erythematosus, thyroiditis, diabetes, uveitis, psoriasis,
XX urticaria, nephrotic syndrome, glomerulonephritis, ulcerative colitis,
XX Crohn's disease, Sjogren's syndrome, toxoplasmosis, listeriosis, leprosy,
XX Lyme disease, tuberculosis, malaria and leishmaniasis. They can also be
XX used for producing antibodies, which can be used for diagnosing diseases.
XX The present sequence represents IL-13 receptor alpha 1 subunit.
XX SQ Sequence 427 AA;
Query Match 100.0%; Score 1760; DB 8; Length 427;
Best Local Similarity 100.0%; Pred. No. 4.1e-164;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRISI 60
DB 27 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRISI 86
QY 61 EVPLNERICLQVGSQCSTNESEKPSILVEKICISPEGDPESAVTELOCIWHNLSYMKCSW 120
DB 87 EVPLNERICLQVGSQCSTNESEKPSILVEKICISPEGDPESAVTELOCIWHNLSYMKCSW 146
QY 121 LPGRTSPDNTYLYWHRSLKIHQCEINIFREQYFGCSPDLTKVKDSSFEQHSVQIMV 180
DB 147 LPGRTSPDNTYLYWHRSLKIHQCEINIFREQYFGCSPDLTKVKDSSFEQHSVQIMV 206
QY 181 KDNAGKIKPSFNIVPLTSRVKPDPPHKNLSFHNDLLVQWENPQNFISRCCLFYEVVNN 240
DB 207 KDNAGKIKPSFNIVPLTSRVKPDPPHKNLSFHNDLLVQWENPQNFISRCCLFYEVVNN 266
QY 241 SOTETHNVFVQAEKACENPERNVNTSCPMVPGVLPDNTLTNTRIRVKTNKLCEYDDKL 300
DB 267 SOTETHNVFVQAEKACENPERNVNTSCPMVPGVLPDNTLTNTRIRVKTNKLCEYDDKL 326
QY 301 WSNWSQEMSIGKKRNSTLYI 320
DB 327 WSNWSQEMSIGKKRNSTLYI 346

RESULT 11
ABM82441
XX ABM82441 standard; protein; 427 AA.
XX AC ABM82441;
XX 18-NOV-2004 (first entry)
XX Tumour-associated antigenic target (TAT) polypeptide PRO2537, SEQ:6271.
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
XX Tumour; diagnosis; cell proliferative disorder; breast cancer;
XX colorectal cancer; lung cancer; ovarian cancer; liver cancer;
XX central nervous system cancer; bladder cancer; pancreatic cancer;
XX
```

KW	cervical cancer; melanoma; leukaemia; hybridisation probe;
KW	chromosome identification; chromosome mapping; gene mapping;
KW	gene therapy; cytostatic.
XX	
OS	Homo sapiens.
XX	
PN	WO2004030615-A2.
XX	
PD	15-APR-2004.
XX	
XX	29-SEP-2003; 2003WO-US028547.
PF	
XX	02-OCT-2002; 2002US-0414971P.
PR	
XX	(GETH) GENENTECH INC.
PA	
XX	Wu TD, Zhang Z, Zhou Y;
PI	
XX	WPI; 2004-347921/32.
XX	N-PSDB; ACN41073.
DR	
XX	
PT	New tumor-associated antigenic target polypeptides and nucleic acids,
PT	useful in preparing a medicament for treating or detecting a
PT	proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT	prostate cancer or tumor.
XX	
PS	Claim 12; SEQ ID NO 6271; 7273pp; English.
XX	
CC	The invention relates to human tumour-associated antigenic target (TAT)
CC	polypeptides, and their related nucleic acids. The TAT polypeptides are
CC	overexpressed in cancer tissues compared to normal tissues, and may thus
CC	serve as effective targets for the diagnosis and treatment of cancer in
CC	mammals. The invention also relates to nucleic acid and polypeptide
CC	sequences at least 80% identical to the TAT nucleic acids and
CC	polypeptides; expression vectors and host cells comprising a TAT nucleic
CC	acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC	molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC	TAT polypeptide; and methods and compositions for the treatment or
CC	diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, useful
CC	antibodies, antagonists, binding molecules and compositions are, useful
CC	for diagnosing or treating a cell proliferative disorder associated with
CC	increased TAT expression, particularly cancers such as breast cancer,
CC	colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC	cancer, pancreatic cancer, cervical cancer, cancers of the central
CC	nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC	used as hybridisation probes, in chromosome and gene mapping, in
CC	chromosome identification and in gene therapy. The present sequence
CC	represents a TAT polypeptide of the invention
XX	
SQ	Sequence 427 AA;
Query Match 100.0%; Score 1760; DB 8; Length 427;	
Best Local Similarity 100.0%; Pred. No. 4.1e-164;	
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 APTETQPPVTNLSVSNLCTVIWTWNPPEGASSNCSLWYFSGHDQDKKIAPETRRSI 60
Db	
Db	27 APTETQPPVTNLSVSNLCTVIWTWNPPEGASSNCSLWYFSGHDQDKKIAPETRRSI 86
Qy	61 EVPLNERICLQVGSQCSTNESEKPSILVEKICISPEGDPESAATVETLQCIWNLSYMKCSW 120
Db	
Db	87 EVPLNERICLQVGSQCSTNESEKPSILVEKICISPEGDPESAATVETLQCIWNLSYMKCSW 146
Qy	121 LPGRNTSPDNTNYLYYHRSLEKIHQCENTIFREGQYFGCSFDLTKVKDSSPEQHSVQIMV 180
Db	
Db	147 LPGRNTSPDNTNYLYYHRSLEKIHQCENTIFREGQYFGCSFDLTKVKDSSPEQHSVQIMV 206
Qy	181 KDNAGKIKPSFNI VPLTSRVKPDPPHINKLSFHNDLLVQWENPNQFTSRCLFYEVEVNN 240
Db	
Db	207 KDNAGKIKPSFNI VPLTSRVKPDPPHINKLSFHNDLLVQWENPNQFTSRCLFYEVEVNN 266
Qy	241 SQTETHNVFYQEAECNPFERNVENTSCMPVPGVLPTDILTIVRIYKTNKLCYEDDKL 300

Db	225	KDNAGKIKPSFNIVPLTSRVKPDPPHIXNLSFHNDLLVQWENQNFISRCLFYEVVNN	284
Qy	241	SQTETHNVFYVOEAKCENPEPERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKL	300
Db	285	SQTETHNVFYVOEAKCENPEPERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKL	344
Qy	301	WSNWSQEMSIGKRNST	317
Db	345	WSNWSQEMSIGKRNST	361

Search completed: February 8, 2006, 21:59:10
Job time : 99.483 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 21:59:28 ; Search time 18.9712 Seconds
(without alignments)
1622.950 Million cell updates/sec

Title: US-10-036-568A-4_COPY_26_345

Perfect score: 1760

Sequence: 1 APETQPPVNLVSVENLCTIWTNPPPGASSNCSLWYFSHFQDKQDKKIAPETRREIEV 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*

- 1: pir1.*
- 2: pir2.*
- 3: pir3.*
- 4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1273.5	72.4	426	2 JC7773	IL-13ralpha 1 prot
2	281	16.0	415	2 S12357	interleukin-5 rece
3	229	13.0	335	2 A40267	interleukin-5 rece
4	228	13.0	420	2 S21052	interleukin-5 rece
5	192	10.9	348	2 JC7907	common cytokine re
6	186.5	10.6	373	2 A55718	interleukin-2 rece
7	181.5	10.3	369	2 A42565	interleukin-2 rece
8	170	9.7	831	2 JQ1655	prolactin receptor
9	168.5	9.6	918	2 A36337	membrane glycoprot
10	162.5	9.2	333	2 S13684	granulocyte-macrop
11	162.5	9.2	400	2 S86945	granulocyte-macrop
12	162	9.2	369	2 I49280	interleukin-2 rece
13	156.5	8.9	378	2 S50040	granulocyte-macrop
14	147.5	8.4	581	2 I45971	prolactin receptor
15	147.5	8.4	616	2 A30304	prolactin receptor
16	147	8.4	1092	2 JX0312	differentiation-st
17	146	8.3	897	1 A32555	cytokine receptor
18	145.5	8.3	830	2 I50455	prolactin receptor
19	145	8.2	396	2 S22909	interleukin-3 rece
20	145	8.2	630	2 I51086	prolactin receptor
21	144	8.2	918	2 A44257	interleukin-6 sign
22	142.5	8.1	896	2 I56563	interleukin-3 rece
23	142.5	8.1	917	2 I49699	glycoprotein l30 -
24	138.5	7.9	310	2 A29884	prolactin receptor
25	138.5	7.9	412	2 A41070	prolactin receptor
26	138.5	7.9	610	2 A34631	lactogen receptor
27	138.5	7.9	610	2 A36116	prolactin receptor
28	138	7.8	896	1 A35782	cytokine receptor
29	138	7.8	1097	2 S17308	leukemia inhibitor

30	136	7.7	878	1 A40091	interleukin-3 rece
31	135.5	7.7	286	2 S50039	granulocyte-macrop
32	130.5	7.4	292	2 I77525	prolactin receptor
33	130.5	7.4	303	2 I77524	prolactin receptor
34	130.5	7.4	608	2 I53269	prolactin receptor
35	130	7.4	288	2 B59405	prolactin receptor
36	130	7.4	376	2 A59405	prolactin receptor
37	130	7.4	622	2 A40144	prolactin receptor
38	123	7.0	378	2 A40266	interleukin-3 rece
39	117	6.6	1471	2 T19506	hypothetical prote
40	116.5	6.6	2029	1 TDFELK	protein-tyrosine-p
41	110.5	6.3	825	1 A60386	interleukin-4 rece
42	108.5	6.2	1268	1 A39640	neural cell adhesi
43	108	6.1	13055	2 T16580	hypothetical prote
44	107	6.1	557	2 A32694	interferon alpha/b
45	106.5	6.1	1259	2 A43425	Bravo/Nr-CAM cell

ALIGNMENTS

RESULT 1

JC7773

IL-13ralpha 1 protein - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C;Accession: JC7773

R;Pierrot, C.; Beniguel, L.; Begue, A.; Khalife, J.

Biochem. Biophys. Res. Commun. 287, 969-976, 2001

A;Title: Expression of a functional IL-13ralpha1 by rat B cells.

A;Reference number: JC7773; PMID:11573960

A;Accession: JC7773

A;Molecule type: mRNA

A;Residues: 1-426 <PIE>

A;Cross-references: UNIPROT:Q8VHC2; UNIPARC:UPI000017CC49; GB:AY044251

C;Comment: This protein is an functionally binding protein involved in B cell proliferat

C;Genetics:

A;Gene: il-13ralpha1

Query Match 72.4%; Score 1273.5; DB 2; Length 426;

Best Local Similarity 72.4%; Pred. No. 1.4e-94;

Matches 231; Conservative 39; Mismatches 46; Indels 3; Gaps 2;

Qy	3	TETQPPVNLVSVENLCTIWTNPPPGASSNCSLWYFSHFQDKQDKKIAPETRREIEV	62
Db	27	TEVQPPVNLVSVENLCTIWTNPPPGASSNCSLWYFSHFQDKQDKKIAPETRREIEV	86
Qy	63	PLNERICLVQSGQCSSTNESEKPSILVEKCI9PPGDPESAATELOCIWHNLSYMKCSWLP	122
Db	87	PLNEKICLVQSGQCSSTNESEKPSPLVKKCI9PPRRGSSAVTELOCTWHNLSYMKCSWLP	146
Qy	123	GRNTSPDNTYLYYWHRSLEKIHQCENTFRGQYFGCSFDLTKKVDSFQHSVOIMVKD	182
Db	147	GRNTSPDNTYLYYWSYSLGKSLQCENTHREGHQHSFKLTKV-ESNYEHNNIQIMVKD	205
Qy	193	NAGTKPSFNVLPTSRVKPPPHIKNL5FHNDLLYQWENPQNFISRCLFYEVENVNSQ	242
Db	206	NAGTKPSYKLVSTSNVVKPPPHIKHLFKNGALFVQWKNPQNFSSRCLSYEVENVNSQ	265
Qy	243	TETH--NVFYVQEAACENPEFERNVENTSCFMPVGLPDLTNTVIRVTKNLCYEDDKL	300
Db	266	TDSYNSNSLVEEDKQCNSEFDRNMEGASCFISPGVLXNTVTVTVRVKTNKLCFDDNDL	325
Qy	301	WSNWSQMSIGKKNRSTLYI 319	
Db	326	WSNWSQMSIGKKNRSTLYI 344	

RESULT 2

S12357

interleukin-5 receptor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

A;Gene: GDB:IL2RG; SCIDX1; IMD4
A;Cross-references: GDB:134807; OMIM:308380
A;Map position: Xq13.1-Xq13.1
A;Introns: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 308/3
A;Note: defects are associated with an X-linked form of severe combined immunodeficiency
C;Superfamily: interleukin-2 receptor gamma chain
C;Keywords: cytokine receptor; duplication; immunodeficiency; transmembrane protein

Query Match 10.3%; Score 181.5; DB 2; Length 369;
Best Local Similarity 26.8%; Pred. No. 5.3e-07;
Matches 61; Conservative 39; Mismatches 87; Indels 41; Gaps 12;

Qy 105 ELQCIWNLNLSVMSKSLPGRNTPSDTNYLYYHRSLL--EKIHQCN-IFREGQYFCSP 161
Db 59 EVQCFFVNEVMNCTWNSSEPOQ-TNLTHLYYKNSDNDKVKQCSHYLFSEETSGC-- 115
Qy 162 DLTKVKDSSFEQHSQVIMVNDNAGKIKPFSNIVPLTSRVKPDPPHINKLSFPH--NDLLY 218
Db 116 QLQKKEIHLQTFVQL--QDPREPRQATQMLKQLNVLVWPAP--ENLTLKLSQSLE 171
Qy 219 VQWENPQNFISRLC-----FYEVVNNSTQTHNVFYVQEAACENPEFERNVENTSCMPVP 274
Db 172 LNNNN--RFLNHCLEHLVQVYRTDWSWT-----EQSDVYRHKFSLP 211
Qy 275 GVLPDTLNTRIRVKTNKLKYEDDKLWSNWSQMSIG---KKNSTLY 319
Db 212 SVDGQKRYTFRVRSRPNLC-GSAQHWSEWSHPHWSNNTSKENPPLF 258

RESULT 8
JQ1555
prolactin receptor precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JQ1655
R;Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A;Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA sequence
A;Reference number: JQ1655; MUID:93075121; PMID:1445292
A;Accession: JQ1655
A;Molecule type: mRNA
A;Residues: 1-831 <TAN>
A;Cross-references: UNIPROT:Q04594; UNIPARC:UPI0000132232; DDBJ:D13154; NID:9222848; PID
A;Experimental source: kidney
C;Keywords: glycoprotein; transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-831/Product: prolactin receptor #status predicted <MAT>
F;36-219/Domain: cytokine receptor homology <CRS1>
F;239-425/Domain: cytokine receptor homology <CRS2>
F;439-462/Domain: transmembrane #status predicted <TM>
F;59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (covalent)

Query Match 9.7%; Score 170; DB 2; Length 831;
Best Local Similarity 23.2%; Pred. No. 1.2e-05;
Matches 79; Conservative 45; Mismatches 137; Indels 80; Gaps 17;

Qy 6 QP--PVTNLSVSVENLCTV--IWT-WNPP--EGASSNCSLWYFHFQDKQKKIAPETRR 58
Db 126 QPGSPV-NLTLETKRSANIYMLAKWSPPLADASN---HLVHY---ELRIKPEKE 176
Qy 59 SIEVPLNERICLVGSCSTNE-----SEKPSILVEKCLSP 95
Db 177 EWET-----ISVGVQTOCKINRLNAGMYVQVVRCTLDPGSEWSERHILIPSGQSP 231
Qy 96 EGDPEAVTELOCIWNLNLSVMSKSLPGRNTPSDTNYLYYHRSLEKIHQCNIPREGQ 155
Db 232 E-----KPTLIKRSPEKFTCWKKQLDGGHPNTNLYLSKEGEQVVECPD-YRTAG 285
Qy 156 YFGCSFDLTQKVDSSFFQHSQVIMVNDNAGKIKPFSNIVPLTSRVKPDPP-----HIKNL 210
Db 286 PMSCYFD--KKHTSFMTIYNTVRATNEMGNSSDPHYVDVTYVQDPDPVNTLELKP 343
Qy 211 SFHNDLLVQWENPQNFISR-----CLFYEVVNNSTQTHNVFYVQEAACENPEFERNVE 266

Db 344 INRKPVLVLTWSPPLADYRSGLTLEYELRLPDEGEWETIFVGQ-QTYKMFSLN-- 400
Qy 267 NTSCFMVPGVLPDTLNTRIRVKTNKLKYEDDKLWSNWSQ 307
Db 401 -----PGKVIQIHCKP-----DHHGWSWSE 425

RESULT 9
A36337
membrane glycoprotein gp130 precursor - human
C;Species: Homo sapiens (man)
C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004
C;Accession: A36337
R;Hibi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.
Cell 63, 1149-1157, 1990
A;Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A;Reference number: A36337; MUID:91084844; PMID:2261637
A;Accession: A36337
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-918 <HIB>
A;Cross-references: UNIPROT:P40189; UNIPARC:UPI0000046B12; GB:M57230; NID:g186353; PID:
C;Genetics:
A;Gene: GDB:IL6ST; GP130
A;Cross-references: GDB:126725; OMIM:600694
A;Map position: 5q11-5q11
C;Keywords: glycoprotein; membrane protein
F;134-316/Domain: cytokine receptor homology <CRS>

Query Match 9.6%; Score 168.5; DB 2; Length 918;
Best Local Similarity 25.3%; Pred. No. 1.9e-05;
Matches 80; Conservative 45; Mismatches 148; Indels 43; Gaps 16;

Qy 6 QPVTNLSVSVENLCTVIMTNPPEGASSNCSLWYFHFQ-DKQKKIAPETRRSIEVPL 64
Db 34 ESPVQLHSNFTAVCLVKEKMDYFHVNANYVWKNHFTPIKEQYTIINRTASVTFTD 93
Qy 65 NERICLVGSCSTNSEKPSILVEKIS--PREGDPESAVTELOCIWNLNLSVMSKSWLP 122
Db 94 IASLNIQLTCNLTFTGQLEQNVYGITISGLPPE-KPKN---LSCIVNEGKMKRCEDWG 148
Qy 123 GRNTSPDTNVL--YYHRSLEKIHQCNIPREGQYFCSPDLTKVKDSSFEQHSQVIMVK 181
Db 149 GRETHLETNFTLKSEW--ATHKFADCK--AKRTPTSCTVDYSTV---YFVNIEVWVEAE 201
Qy 182 DNAGKI-KPSFNIVPLTSRVKPDPPHINKLSFPHND-----LYVQWENPQNFISRLCFYE 235
Db 202 NALGKVTSDHINFDVP-YKVKPNPPH--NLSVINSELSILKLTWNPISIKSVIILKYN 258
Qy 236 VEYVNSQTETHNVFYVQEAACENPEFERNVENTSCFMPVPGVLPDTLNTRIRVKTNKLKY 295
Db 259 IQVTKDASTWS-----QIPP-EDTASTRSSFTVDLKPFTYVFRIR-----CM 302
Qy 296 EDD--KLWSNWSQMS 309
Db 303 KEDGKGYSWDSSEAS 318

RESULT 10
S13684
granulocyte-macrophage colony-stimulating factor receptor - human
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S13684; A40989
R;Ashworth, A.; Kraft, A.
Nucleic Acids Res. 18, 7178, 1990
A;Title: Cloning of a potentially soluble receptor for human GM-CSF.
A;Reference number: S13684; MUID:91088339; PMID:2148207
A;Accession: S13684
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-333 <ASH>

A;Cross-references: UNIPROT:P15509; UNIPARC:UPI000002AAA1; EMBL:X54935; NID:G31860; PIDN:R;Raines, M.A.; Liu, L.; Qian, S.G.; Joe, V.; Dipersio, J.F.; Golde, D.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 8203-8207, 1991
A;Title: Identification and molecular cloning of a soluble human granulocyte-macrophage
A;Reference number: A40989; MUID:91376112; PMID:1832774
A;Accession: A40989
A;Molecule type: mRNA
A;Residues: 314-333 <RAI>
A;Cross-references: UNIPARC:UPI0000017C140; GB:M73832

Query Match 9.2%; Score 162.5; DB 2; Length 333;
Best Local Similarity 20.5%; Pred. No. 1.6e-05;
Matches 65; Conservative 61; Mismatches 152; Indels 39; Gaps 12;

Qy 5 TOPPVNLVSUENLCTVIWNTNPPGAS--SNCSLMWFSHFHGDQKDKKIAPETRRSIEVP 63
Db 29 TVAPASSLNVRFSR--TNMNSWDCQENTTFKCFI-----TDKKNRVVEPRLSNNECS 81

Qy 64 LNERICLVGSCSTNSEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSWMLPG 123
Db 82 TFRICLHEGVTFEVHNTSQRGQOKLLYPNSGREGTAQNFCFIYNADLMNCTWARG 141

Qy 124 RNTSPDNTYLYWHRSLEKIQHCENIFRE--GOYFGCSFD--LTKVKDSSPEQHSVQIMVK 181
Db 142 PTAPRDVQVFLYIRNSKRREIRCPYYIQDSGTHVGHCHLDNLGLTSRNY-----FLVN 195

Qy 182 DNACKIKPSP--NIVPLTSRVKPDPPHINKLSFNDDLYVQWENPQNF--ISRCLF--YEV 236
Db 196 GTSREIGIQFDSLLDTKKIERFPNPNVTRCNTHCLVRWKQPTVQKLSYLDQFQOL 255

Qy 237 EVN--NSQTEHNVFYVQEAECNPEFERNVENTSCFMPGVGLPDLTNTVIRVKTNKL 294
Db 256 DVHRKNTQGTENLLINVGDLNR-----YNFSPSEPRKHSVKIRAADVRIL 304

Qy 295 YEDDKLWSNQSEMSIG 311
Db 305 N-----WSSWSEAIIEFG 316

RESULT 11

S06945
granulocyte-macrophage colony-stimulating factor receptor A precursor - human
N;Alternate names: GM-CSF receptor alpha chain; hemopoietic growth factor receptor
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence revision 22-Jan-1993 #text_change 09-Jul-2004
C;Accession: S06945; A41286; A44474
R;Geating, D.P.; King, J.A.; Gough, N.M.; Nicola, N.A.
EMBO J. 8, 3667-3676, 1989
A;Title: Expression cloning of a receptor for human granulocyte-macrophage colony-stimul
A;Reference number: S06944; MUID:90059966; PMID:2555171
A;Accession: S06945
A;Molecule type: mRNA
A;Residues: 1-400 <GEA>
A;Cross-references: UNIPROT:P15509; UNIPARC:UPI0000000C45; EMBL:X17648; NID:G32087; PIDN
R;Crosier, K.E.; Wong, G.G.; Mathey-Prevot, B.; Nathan, D.G.; Sieff, C.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 7744-7748, 1991
A;Title: A functional isoform of the human granulocyte/macrophage colony-stimulating fac
A;Reference number: A41286; MUID:91352066; PMID:1715577
A;Accession: A41286
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 347-400 <CRO>
A;Cross-references: UNIPARC:UPI000017C141
R;Rappold, G.; Willison, T.A.; Henke, A.; Gough, N.M.
Genomics 14, 455-461, 1992
A;Title: Arrangement and localization of the human GM-CSF receptor alpha chain gene CSF2
A;Reference number: A44474; MUID:93052350; PMID:1358805
A;Accession: A44474
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 'M', 377-400 <RAP>
A;Cross-references: UNIPARC:UPI00000723FC; GB:S48539; NID:G258858; PIDN:AAB23942.1; PID:
A;Note: sequence extracted from NCBI backbone (NCBI:P117980)

C;Genetics:
A;Gene: GDB:CSF2RA; CSF2R
A;Cross-references: GDB:I118777; OMIM:306250; OMIM:425000
A;Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
C;Keywords: glycoprotein; growth factor receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-400/Product: granulocyte-macrophage colony-stimulating factor receptor #status pred
F;322-346/Domain: transmembrane #status predicted <TM>
F;46,54,99,123,135,182,195,223,229,272,305/Binding site: carbohydrate (Asn) (covalent) #

Query Match 9.2%; Score 162.5; DB 2; Length 400;
Best Local Similarity 20.5%; Pred. No. 2e-05;
Matches 65; Conservative 61; Mismatches 152; Indels 39; Gaps 12;

Qy 5 TOPPVNLVSUENLCTVIWNTNPPGAS--SNCSLMWFSHFHGDQKDKKIAPETRRSIEVP 63
Db 29 TVAPASSLNVRFSR--TNMNSWDCQENTTFKCFI-----TDKKNRVVEPRLSNNECS 81

Qy 64 LNERICLVGSCSTNSEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSWMLPG 123
Db 82 TFRICLHEGVTFEVHNTSQRGQOKLLYPNSGREGTAQNFCFIYNADLMNCTWARG 141

Qy 124 RNTSPDNTYLYWHRSLEKIQHCENIFRE--GOYFGCSFD--LTKVKDSSPEQHSVQIMVK 181
Db 142 PTAPRDVQVFLYIRNSKRREIRCPYYIQDSGTHVGHCHLDNLGLTSRNY-----FLVN 195

Qy 182 DNACKIKPSP--NIVPLTSRVKPDPPHINKLSFNDDLYVQWENPQNF--ISRCLF--YEV 236
Db 196 GTSREIGIQFDSLLDTKKIERFPNPNVTRCNTHCLVRWKQPTVQKLSYLDQFQOL 255

Qy 237 EVN--NSQTEHNVFYVQEAECNPEFERNVENTSCFMPGVGLPDLTNTVIRVKTNKL 294
Db 256 DVHRKNTQGTENLLINVGDLNR-----YNFSPSEPRKHSVKIRAADVRIL 304

Qy 295 YEDDKLWSNQSEMSIG 311
Db 305 N-----WSSWSEAIIEFG 316

RESULT 12

I49280
interleukin-2 receptor gamma chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Feb-1997 #sequence revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: I49280; A47514; JN0592; JN0775; S37582; I53398
R;Cao, X.; Kozak, C.A.; Liu, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993
A;Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R) ga
A;Reference number: A47514; MUID:93391374; PMID:8378320
A;Accession: I49280
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-369 <CAO>
A;Cross-references: UNIPROT:P34902; UNIPARC:UPI00000001949; EMBL:U21795; NID:G727349; PID
A;Accession: A47514
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-369 <RE2>
A;Cross-references: UNIPARC:UPI00000001949; GB:L20048; NID:G404067; PIDN:AAA39286.1; PID:
R;Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamura, K.
Biochem. Biophys. Res. Commun. 193, 356-363, 1993
A;Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of func
A;Reference number: JN0592; MUID:93277575; PMID:8503926
A;Accession: JN0592
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-369 <KUM>
A;Cross-references: UNIPARC:UPI00000001949; DBJ:D13565; NID:G303684; PIDN:BAA02760.1; PI
R;Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.
Gene 130, 303-304, 1993
A;Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.
A;Reference number: JN0775; MUID:93366191; PMID:8359699
A;Accession: JN0775

Job time : 19.9712 secs

Db	70	TLIECPD-YKGGPNSCF--SKKHTSIWKVYITVNAINQMGISSSDPLYVHVTVIVE	126
Qy	202	PDPPHKNLSF---HNDD---LVQWENPON-----FISRCIFYEVEVNSQT---E	244
Db	127	PEPP--ANLTLKHPEDRKPYLMIKMSPTTIDVKSGWFI---IQYEIRLKPEKATDWE	181
Qy	245	THNVFYQEAKECENPEPERNVENTSCFMVPGVLPDPLTNTVRIRVKTNKLGYEDDDKLMSNW	304
Db	182	THFTLKOTQLKIFN-----LYPQKYLQVIR-----CKPDHGYWSEW	218
Qy	305	SQEMSI 310	
Db	219	SPSSI 224	
RESULT 15			
A30304			
prolactin receptor 2 precursor - rabbit			
N;Alternate names: prolactin receptor, mammary gland			
C;Species: Oryctolagus cuniculus (domestic rabbit)			
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004			
C;Accession: A30304; A60380			
R;Entry, M.; Jolicoeur, C.; Levi-Meyrueis, C.; Dusanter-Fourt, I.; Petridou, B.; Boutin, Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989			
A;Title: Identification and sequence analysis of a second form of prolactin receptor by			
A;Reference number: A30304; MUID:89184578; PMID:2928321			
A;Accession: A30304			
A;Molecule type: mRNA			
A;Residues: 1-616 <EDS>			
A;Cross-references: UNIPROT:P14787; UNIPARC:UPI0000132237; GB:J04510; NID:G165669; PIDN:			
R;Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.			
Int. J. Biochem. 22, 1089-1095, 1990			
A;Title: Purification and partial sequence of the rabbit mammary gland prolactin recepto			
A;Reference number: A60380; MUID:91146782; PMID:2289615			
A;Accession: A60380			
A;Molecule type: protein			
A;Residues: 41-58, 'X', 60-66; 90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NK', 108, 150-164, 'XX', 167			
A;Cross-references: UNIPARC:UPI000017C5D9; UNIPARC:UPI000017C5DA; UNIPARC:UPI000017C5DB;			
A;Note: the amino end of the mature protein was blocked			
C;Keywords: blocked amino end; glycoprotein; transmembrane protein			
P;1-24/Domain: signal sequence #status predicted <SIG>			
F;25-616/Product: prolactin receptor 2 #status predicted <WAT>			
F;36-221/Domain: cytokine receptor homology <CRS>			
F;235-258/Domain: transmembrane #status predicted <TM>			
F;59,104,132,347,389,411/Binding site: carbohydrate (Asn) (covalent) #status predicted			
Query Match 8.4%; Score 147.5; DB 2; Length 616;			
Best Local Similarity 26.7%; Pred. No. 0.00055;			
Matches 65; Conservative 29; Mismatches 86; Indels 63; Gaps 14;			
Qy	83	KPSILVKEKISPPGDPESAVTELCQIWHNLSYMKCSMLPGRNTSPDTNYTLYYWHSLE	142
Db	30	KPFIP--KCRSEK-----BTFTCWRRPGADGGGLPTNYLTLY-HKEGE	69
Qy	143	KI-HOCENIFREGQVFGSGFDLTQKVDSSFEQHSVQIWKDAGKIKPSFNIVPLTSRVK	201
Db	70	TIITHECPD-YKGGPNSCF--SKKHTSIWTIYIITVATNQMSSVSDPRYVDVTVIVE	126
Qy	202	PDPPHKNLSF---HNDD---LVQWENPONFISR---CLFYEVFV---NNSQETETHN	247
Db	127	PDPP--VNLTLVKHPEDRKPYLWKVWLPDPLTVDRSGWLTQYELRLKPEKAAEWETH-	183
Qy	248	VFYVQEAKECENPEPERNVENTSCFMVPGVLPDPLTNTVRIRVKTNKLGYEDDDKLMSNWSQE	307
Db	184	-FAGQQTQ-----FKLSLYPQKYLQVIR-----CKPDHGFWSVWSPE	221
Qy	308	MSI 310	
Db	222	SSI 224	

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 21:53:18 ; Search time 111.316 Seconds
(without alignments)
2028.173 Million cell updates/sec

Title: US-10-036-568A-4_COPY_26_345

Perfect score: 1760

Sequence: 1 APETQPVNLSVSNELC.....WSNWSQEMSGKKENSTLYI 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05_80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No! is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1760	100.0	427	1 I13R1_HUMAN	P78552 homo sapien
2	1760	100.0	427	2 Q5JSL4_HUMAN	Q5JSL4 homo sapien
3	1760	100.0	427	2 Q96BB4_HUMAN	Q96BB4 homo sapien
4	1747	99.3	426	2 Q59EG2_HUMAN	Q59EG2 homo sapien
5	1692	96.1	409	2 Q7YRV5_MACACA	Q7YRV5 macaca fasc
6	1532	87.0	401	2 Q6U6T1_SHEEP	Q6U6T1 ovis aries
7	1478	84.0	405	2 Q95LF1_CANFA	Q95LF1 canis faml
8	1465.5	83.3	423	2 Q863Z6_PIG	Q863Z6 sus scrofa
9	1444	82.0	349	2 Q97597_BOVIN	Q97597 bos taurus
10	1387	78.8	279	2 Q9UDY5_HUMAN	Q9UDY5 homo sapien
11	1314.5	74.7	424	1 I13R1_MOUSE	O09030 mus musculus
12	1308.5	74.3	424	2 Q8C1Z3_MOUSE	Q8C1Z3 mus musculus
13	1307.5	74.3	426	2 Q561K3_RAT	Q561K3 rattus norv
14	1302.5	74.0	424	2 Q8BNM4_MOUSE	Q8BNM4 mus musculus
15	1274.5	72.4	426	2 Q8VHC2_RAT	Q8VHC2 rattus norv
16	603.5	34.3	252	2 Q8VDP7_MOUSE	Q8VDP7 mus musculus
17	296	16.8	386	1 I13R2_CANFA	Q951F0 canis faml
18	284	16.1	380	1 I13R2_HUMAN	Q14627 homo sapien
19	281	16.0	415	1 IL5R2_MOUSE	P21183 mus musculus
20	278	15.8	383	2 Q88786_MOUSE	Q88786 mus musculus
21	267	15.2	385	2 Q8VHK6_RAT	Q8VHK6 rattus norv
22	253	14.4	391	2 Q6UAN8_TETNG	Q6UAN8 tetraodon n
23	239	13.6	393	2 Q5U516_XENLA	Q5U516 xenopus lae
24	235.5	13.4	415	2 Q920K4_CAVPO	Q920K4 cavia porce
25	235	13.4	414	2 Q920B8_RAT	Q920B8 rattus norv
26	234	13.3	414	2 Q99PS3_RAT	Q99PS3 rattus norv
27	233	13.2	404	2 Q90XP8_ONCMY	Q90XP8 oncorhynch
28	230	13.1	420	1 IL5RA_HUMAN	Q01344 homo sapien
29	229	13.0	333	2 Q15469_HUMAN	Q15469 homo sapien
30	228	13.0	420	2 Q14633_HUMAN	Q14633 homo sapien
31	227	12.9	396	2 Q14631_HUMAN	Q14631 homo sapien

RESULT 1

ID	I13R1_HUMAN	STANDARD;	PRT;	427 AA.
AC	P78552; Q95646; Q9656;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-13RA-1) (CD213al antigen).			
DE	13RA-1) (CD213al antigen).			
GN	Name=IL13RA1; Synonyms=IL13R, IL13RA;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Carcinoma;			
RX	MEDLINE=97165986; PubMed=9013879; DOI=10.1016/S0014-5793(96)01462-7;			
RA	Miloux B., Laurent P., Bonnin O., Lupker J., Caput D., Vita N.,			
RA	Ferrara P.;			
RT	"Cloning of the human IL-13R alpha chain and reconstitution with the			
RT	IL4R alpha of a functional IL-4/IL-13 receptor complex.";			
RL	FEBS Lett. 401:163-166(1997).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=B-cell;			
RA	Gauchat J.F.M., Schlagenhaut E., Peng N.P., Moser R., Yanage M.,			
RA	Jearnin P., Alouani S., Elson G., Notarangelo L.D., Wells T.,			
RA	Eugster H.P., Bonnefoy J.Y.;			
RL	Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=T-cell;			
RX	MEDLINE=97067184; PubMed=8910586; DOI=10.1074/jbc.271.46.29285;			
RA	Aman M.J., Tayebi N., Obiri N.I., Puri R.K., Modi W.S., Leonard W.J.;			
RT	"cDNA cloning and characterization of the human interleukin 13			
RT	receptor alpha chain.";			
RL	J. Biol. Chem. 271:29265-29270(1996).			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Wada M., Hisano T., Kuwano M.;			
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].			
RC	TISSUE=Pancreas;			
RX	MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			

ALIGNMENTS

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vallalao D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Raha J.J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc Natl Acad Sci U S A. 99:16999-16903(2002).
 CC -I- FUNCTION: Binds IL13 with a low affinity. Together with IL4R-alpha
 CC can form a functional receptor for IL13. Also serves as an
 CC alternate accessory protein to the common cytokine receptor gamma
 CC chain for IL4 signaling, but cannot replace the function of gamma
 CC C in allowing enhanced IL2 binding activity.
 CC -I- SUBUNIT: Interleukin 13 receptor is a complex of IL4R, IL13RA1,
 CC and possibly other components.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -I- TISSUE SPECIFICITY: Ubiquitous. Highest levels in heart, liver,
 CC skeletal muscle and ovary; lowest levels in brain, lung and
 CC kidney. Also found in B-cells, T-cells and endothelial cells.
 CC -I- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding.
 CC -I- DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation.
 CC -I- SIMILARITY: Belongs to the type I cytokine receptor family. Type 5
 CC subfamily.

 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

 DR ENBL; Y10659; CAA71669.1; -; mRNA.
 DR ENBL; Y09328; CAA70508.1; -; mRNA.
 DR ENBL; U62858; AAB37127.1; -; mRNA.
 DR ENBL; U81379; AAD00510.3; -; mRNA.
 DR ENBL; BC009960; AAH09960.1; -; mRNA.
 DR Ensembl; ENSG00000131724; Homo sapiens.
 DR HGNC; HGNC:5974; IL13RA1.
 DR H-InvDB; HIX0017008; -.
 DR MIM; 300119; -.
 DR GO; GO:0005898; C:plasma membrane; TAS.
 DR GO; GO:0005886; P:cell surface receptor linked signal transdu. . . ; TAS.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . . ; TAS.
 DR InterPro; IPR002996; Cytok_recept_B/G.
 DR InterPro; IPR003532; Hemtptnrecept_F2.
 DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
 KW Glycoprotein; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 21 Potential
 FT CHAIN 22 427 Interleukin-13 receptor alpha-1 chain.
 FT TOPO_DOM 22 343 Extracellular (Potential).
 FT TRANSMEM 344 367 Potential.
 FT TOPO_DOM 368 427 Cytoplasmic (Potential).
 FT MOTIF 327 331 WSXWS motif.
 FT MOTIF 374 382 Box 1 motif.
 FT CARBOHYD 37 37 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 61 61 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 105 105 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 138 138 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 157 157 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 235 235 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 265 265 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 293 293 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 329 329 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 341 341 N-linked (GlcNAc. . .) (Potential).
 FT DISULFID 46 95 Potential.
 FT DISULFID 134 144 By similarity.

FT DISULFID 173 185 By similarity.
 FT CONFLICT 130 130 T -> I (in Ref. 3).
 FT CONFLICT 358 358 G -> D (in Ref. 3).
 SQ SEQUENCE 427 AA; 48760 MW; 5983B3B8F554107B CRC64;
 Query Match 100.0%; Score 1760; DB 1; Length 427;
 Best Local Similarity 100.0%; Pred. No. 6.3e-130;
 Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APTETQPPVTNLSVSVENLCTVIWTPNPPGASSNCSLMWYFSGDKQDKKIAPETRRSI 60
 DB 27 APTETQPPVTNLSVSVENLCTVIWTPNPPGASSNCSLMWYFSGDKQDKKIAPETRRSI 86
 QY 61 EYPLNERICLVGSCQSTNESEKPSILVKEKISPPGDPESATELQCIWHNLSYMKCSW 120
 DB 87 EYPLNERICLVGSCQSTNESEKPSILVKEKISPPGDPESATELQCIWHNLSYMKCSW 146
 QY 121 LPRGNTSPDTNLTLYYWHRSLEKIHOCENIFRGGQVFGCSFDLTVKVDSFQHSVQIMV 180
 DB 147 LPRGNTSPDTNLTLYYWHRSLEKIHOCENIFRGGQVFGCSFDLTVKVDSFQHSVQIMV 206
 QY 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLYVQWENPQNPFISRCIFYEVEVNN 240
 DB 207 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLYVQWENPQNPFISRCIFYEVEVNN 266
 QY 241 SQTETHNVFYQBAKCNPEFERNVENTSCFMVPGVLPTLNTVTRVTKNKLCEYDDKL 300
 DB 267 SQTETHNVFYQBAKCNPEFERNVENTSCFMVPGVLPTLNTVTRVTKNKLCEYDDKL 326
 QY 301 WSNWSQEMSIGKKRNSTLYI 320
 DB 327 WSNWSQEMSIGKKRNSTLYI 346
 RESULT 2
 ID Q5JSL4_HUMAN PRELIMINARY; PRT; 427 AA.
 AC Q5JSL4;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Interleukin 13 receptor, alpha 1.
 GN Name=IL13RA1; ORFNames=RP13-12804.2-001;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Lawlor S.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -I- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding (By similarity).
 CC -I- DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation (By similarity).
 CC EMBL; AL391280; CAI41410.1; -; Genomic_DNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . . ; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR002996; Cytok_recept_B/G.
 DR InterPro; IPR003532; Hemtptnrecept_F2.
 DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
 KW Receptor; Transmembrane.
 SQ SEQUENCE 427 AA; 48760 MW; 5983B3B8F554107B CRC64;
 Query Match 100.0%; Score 1760; DB 2; Length 427;
 Best Local Similarity 100.0%; Pred. No. 6.3e-130;
 Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APTETQPPVTNLSVSVENLCTVIWTPNPPGASSNCSLMWYFSGDKQDKKIAPETRRSI 60

Db 27 APTETQPPVNTLSVSVENLCTVIWTPNPPEGASNCSLWYFHFHGDQKDKKIAPETRRSI 86
Qy 61 EVPLNERICLVQVQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 120
Db 87 EVPLNERICLVQVQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 146
Qy 121 LPGRNTSPDNTYLYYWHRSLEKIHQCENIPREGQYFGCSPDLTKVKDSSFEQHSVQIMV 180
Db 147 LPGRNTSPDNTYLYYWHRSLEKIHQCENIPREGQYFGCSPDLTKVKDSSFEQHSVQIMV 206
Qy 181 KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLLVQWENPQNFISRCIFYEVEVNN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLLVQWENPQNFISRCIFYEVEVNN 266
Qy 241 SQTETHNVFYVQEAKECENPEPERNVNTSCFMVPGVLPDNTLVIRVKTNKLCEYEDDKL 300
Db 267 SQTETHNVFYVQEAKECENPEPERNVNTSCFMVPGVLPDNTLVIRVKTNKLCEYEDDKL 326
Qy 301 WSNWSQEMSIGKGRNSTLYI 320
Db 327 WSNWSQEMSIGKGRNSTLYI 346

RESULT 3
Q96BB4_HUMAN
ID Q96BB4_HUMAN PRELIMINARY; PRT; 427 AA.
AC Q96BB4; Q9WX08;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Interleukin 13 receptor, alpha 1.
GN Name=IL13RA1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBSJ databases.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).

DR EMBL; BC015768; AAH15768.1; -, mRNA.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016020; C: membrane; IEA.
DR GO; GO:0004896; P: hematopoietin/interferon-class (D200-domain. . .); IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR InterPro; IPR002996; Cytok_recept_B/G.
DR InterPro; IPR003532; Hemtptnrecept_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 427 AA; 48677 MW; E6A42F7466A39A09 CRC64;
Query Match 100.0%; Score 1760; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 6.3e-130;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 APTETQPPVNTLSVSVENLCTVIWTPNPPEGASNCSLWYFHFHGDQKDKKIAPETRRSI 60
Db 27 APTETQPPVNTLSVSVENLCTVIWTPNPPEGASNCSLWYFHFHGDQKDKKIAPETRRSI 86
Qy 61 EVPLNERICLVQVQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 120
Db 87 EVPLNERICLVQVQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 146
Qy 121 LPGRNTSPDNTYLYYWHRSLEKIHQCENIPREGQYFGCSPDLTKVKDSSFEQHSVQIMV 180
Db 147 LPGRNTSPDNTYLYYWHRSLEKIHQCENIPREGQYFGCSPDLTKVKDSSFEQHSVQIMV 206
Qy 181 KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLLVQWENPQNFISRCIFYEVEVNN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLLVQWENPQNFISRCIFYEVEVNN 266
Qy 241 SQTETHNVFYVQEAKECENPEPERNVNTSCFMVPGVLPDNTLVIRVKTNKLCEYEDDKL 300
Db 267 SQTETHNVFYVQEAKECENPEPERNVNTSCFMVPGVLPDNTLVIRVKTNKLCEYEDDKL 326
Qy 301 WSNWSQEMSIGKGRNSTLYI 320
Db 327 WSNWSQEMSIGKGRNSTLYI 346

RESULT 4
Q59EG2_HUMAN
ID Q59EG2_HUMAN PRELIMINARY; PRT; 426 AA.
AC Q59EG2;
DT 10-MAY-2005 (TremBLrel. 30, Created)
DT 10-MAY-2005 (TremBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TremBLrel. 30, Last annotation update)
DE Interleukin 13 receptor, alpha 1 variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Aorta endothelial cell;
RA Tokoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
Ohara O., Nagase T., Kikuno F.R.;
RT "None Title."
RL Submitted (MAR-2005) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AB209849; BAD93086.1; -, mRNA.
KW Receptor.
FT NON_TER
SQ SEQUENCE 426 AA; 48555 MW; 342A3A6F7347261B CRC64;
Query Match 99.3%; Score 1747; DB 2; Length 426;
Best Local Similarity 99.7%; Pred. No. 6.6e-129;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 APTETQPPVNTLSVSVENLCTVIWTPNPPEGASNCSLWYFHFHGDQKDKKIAPETRRSI 60
Db 26 APTETQPPVNTLSVSVENLCTVIWTPNPPEGASNCSLWYFHFHGDQKDKKIAPETRRSI 85

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QY 61 EVPLNERICLVGSCQSTNESEKPSILVEKCI SPPEGDPSAVTELCQIWHNLSYMKCSW 120
Db 86 EVPLNERICLVGSCQSTNESEKPSILVEKCI SPPEGDPSAVTELCQIWHNLSYMKCSW 145
QY 121 LPGRNTSPDNTYLYWHRSLKIHQENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 180
Db 146 LPGRNTSPDNTYLYWHRSLKIHQENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 205
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLQYQWENPQNFI SRCLFYFEVEVNN 240
Db 206 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLQYQWENPQNFI SRCLFYFEVEVNN 265
QY 241 SQTEHNVFVQAKCENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKL CYEDDKL 300
Db 266 SQTEHNVFVQAKCENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKL CYEDDKL 325
QY 301 WSNWSQEMSIGKKRNSTLYI 320
Db 326 WSNWSQEMSIGKKRNSTLYI 345

RESULT 5
Q7YRV5 MACFA
ID Q7YRV5 MACFA PRELIMINARY; PRT; 409 AA.
AC Q7YRV5
DT 01-OCT-2003 (TReMBUrel. 25, Created)
DT 01-OCT-2003 (TReMBUrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBUrel. 26, Last annotation update)
DE Interleukin 13 receptor alpha 1 (Fragment).
GN Name=IL13ral;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Maccarone P., Drinkwater C.C., Nash A.D.;
RT "Cynomolgus monkey interleukin 13 receptor alpha 1.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY312267; AAP78901.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytokn_recept_B/G.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003532; Hemtptnrecept_F2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor.
FT CHAIN 9 409 interleukin 13 receptor alpha 1.
FT NON_TER 1
SQ SEQUENCE 409 AA; 46685 MW; 9B98A52671686AF4 CRC64;

Query Match 96.1%; Score 1692; DB 2; Length 409;
Best Local Similarity 95.9%; Pred. No. 1.3e-124;
Matches 307; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 1 APTEOPPVTNLSVSVENLCTVIWTPNPPGASNCSLYFHFSGDKQDKKIAPETRRI 60
Db 9 APTEOPPVTNLSVSVENLCTVIWTPNPPGASNCSLYFHFSGDKQDKKIAPETRRI 68
QY 61 EVPLNERICLVGSCQSTNESEKPSILVEKCI SPPEGDPSAVTELCQIWHNLSYMKCSW 120
Db 69 EVPLNERICLVGSCQSTNESEKPSILVEKCI SPPEGDPSAVTELCQIWHNLSYMKCSW 128
QY 121 LPGRNTSPDNTYLYWHRSLKIHQENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 180
Db 129 LPGRNTSPDNTYLYWHRSLKIHQENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 188
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLQYQWENPQNFI SRCLFYFEVEVNN 240
Db 189 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLQYQWENPQNFI SRCLFYFEVEVNN 248
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QY 241 SQTEHNVFVQAKCENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKL CYEDDKL 300
Db 249 SQTEHNVFVQAKCENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKL CYEDDKL 308
QY 301 WSNWSQEMSIGKKRNSTLYI 320
Db 309 WSNWSQEMSIGKKRNSTLYI 328
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RESULT 6

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Q6U6T1 SHEEP
ID Q6U6T1 SHEEP PRELIMINARY; PRT; 401 AA.
AC Q6U6T1
DT 05-JUL-2004 (TReMBUrel. 27, Created)
DT 05-JUL-2004 (TReMBUrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBUrel. 27, Last annotation update)
DE Interleukin 13 receptor alpha 1 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Maccarone P., Drinkwater C.C., Nash A.D.;
RT "Cloning of the sheep interleukin 13 receptor alpha 1 cDNA.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY377582; AAQ83584.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytokn_recept_B/G.
DR InterPro; IPR003532; Hemtptnrecept_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor.
FT CHAIN <1 401 interleukin 13 receptor alpha 1.
FT NON_TER 1
SQ SEQUENCE 401 AA; 45834 MW; 4E7AD6162BD42B25 CRC64;
```

Query Match 87.0%; Score 1532; DB 2; Length 401;
Best Local Similarity 86.2%; Pred. No. 4.8e-112;
Matches 276; Conservative 17; Mismatches 27; Indels 0; Gaps 0;

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QY 1 APTEOPPVTNLSVSVENLCTVIWTPNPPGASNCSLYFHFSGDKQDKKIAPETRRI 60
Db 1 APAESHPVTNLSVSVENLCTVIWTPNPPGASNCSLYFHFSGDKQDKKIAPETRRI 60
QY 61 EVPLNERICLVGSCQSTNESEKPSILVEKCI SPPEGDPSAVTELCQIWHNLSYMKCSW 120
Db 61 EVPLNERICLVGSCQSTNESEKPSILVEKCI SPPEGDPSAVTELCQIWHNLSYMKCSW 120
QY 121 LPGRNTSPDNTYLYWHRSLKIHQENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 180
Db 121 LPGRNTSPDNTYLYWHRSLKIHQENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 180
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLQYQWENPQNFI SRCLFYFEVEVNN 240
Db 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLQYQWENPQNFI SRCLFYFEVEVNN 240
QY 241 SQTEHNVFVQAKCENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKL CYEDDKL 300
Db 241 SHAETHDIFVYBEAKCQNTPEFERNLEGTICFMVPGVLPDTLNTVIRVKTNKL CYEDDKL 300
QY 301 WSNWSQEMSIGKKRNSTLYI 320
Db 301 WSNWSQEMSIGKANPTFYI 320
```

RESULT 7

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Q95LF1 CANFA
ID Q95LF1 CANFA PRELIMINARY; PRT; 405 AA.
AC Q95LF1;
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DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DB Interleukin 13 receptor alpha chain 1 (fragment).
GN Name=IL13Rai;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=21287533; PubMed=11389954; DOI=10.1016/S0165-2427(01)00271-9;
RA Tang L.;
RT "Molecular cloning of canine IL-13 receptor alpha chain (alpha1 and alpha2) cDNAs and detection of corresponding mRNAs in canine tissues.";
RL Vet. Immunol. Immunopathol. 79:181-195(2001).
DR EMBL; AF314532; AAL14886.1; -; mRNA.
DR Ensembl; ENSCAFG00000018359; Canis familiaris.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytkn recept_B/G.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003532; Hemtptnrecept_F2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor.
FT NON TER.
SQ SEQUENCE 405 AA; 46328 MW; 926E1AC7BE5B3F42 CRC64;

Query Match 84.0%; Score 1478; DB 2; Length 405;
Best Local Similarity 83.4%; Pred. No. 8.6e-108;
Matches 267; Conservative 22; Mismatches 31; Indels 0; Gaps 0;

QY 1 APTETQPPVNLVSVENLCTVIWTPNPPEGASNCSLWYFHFSGDKDKKIAPETRRSI 60
DB 5 APTETQPPVNLVSVENLCTVIWTPNPPEGASNCSLWYFHFSGDKDKKIAPETRRSK 64
QY 61 EVPLNERICLVGSGCSTNSEDNPSILVEKICISPPGDPESAVTELOQIWHNLSYMKCSW 120
DB 65 EVPLNERICLVGSGCSTNSEDNPSILVEKICISPPGDPESAVTELOQIWHNLSYMKCTW 124
QY 121 LPRNTSPDNTYLYYHRSLEKIHQENIFREGYFCGSDLTAKVDSSFEQHSVQIMV 180
DB 125 LPRNTSPDNTYLYYHRSLEKIHQENIFREGYFCGSDLTAKVDSSFEQHSVQIMV 184
QY 181 KDNAGKIPSNIVPLTSRVKPDPPHINKLSFHNDDLYVQWENPQNFISRCIFYEVEVNN 240
DB 185 KDNARKIPSNIVPLTSRVKPDPPHINKLRFQNGNLYVQWKNPQNFISRCILSYQVEVNN 244
QY 241 SQTETHNVFYVQEAACENPEPERNVENTSCFMPVPGVLPDNTLVIRVKTNKLCEYDDKL 300
DB 245 SQTETHNVFYVQEAACENPEPERNVENTSCFMPVPGVLPDNTLVIRVKTNKLCEYDDKL 304
QY 301 WSNWSQMSIGKRNSTLYI 320
DB 305 WSNWSQMSIGKRNSTLYI 324

RESULT 8
Q86326_PIG
ID Q86326_PIG PRELIMINARY; PRT; 423 AA.
AC Q86326;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin 13 receptor alpha 1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.

OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15350752; DOI=10.1016/j.vetimm.2004.05.003;
RA Zarlega D.S., Dawson H., Krangel H., Solano-Aguilar G., Urban J.F. Jr.;
RT "Molecular cloning of the Swine IL-4 receptor alpha and IL-13 receptor 1-chains: effects of experimental Toxoplasma gondii, Ascaris suum and Trichuris suis infections on tissue mRNA levels.";
RL Vet. Immunol. Immunopathol. 101:223-234(2004).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- DOMAIN: The WSWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding (By similarity).
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or activation (By similarity).
DR EMBL; AY266142; AAP23301.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytkn recept_B/G.
DR InterPro; IPR003532; Hemtptnrecept_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 423 AA; 47984 MW; EA636FE6B8CA533D9 CRC64;

Query Match 83.3%; Score 1465.5; DB 2; Length 423;
Best Local Similarity 82.5%; Pred. No. 8.8e-107;
Matches 264; Conservative 23; Mismatches 32; Indels 1; Gaps 1;

QY 1 APTETQPPVNLVSVENLCTVIWTPNPPEGASNCSLWYFHFSGDKDKKIAPETRRSI 60
DB 24 APTETQPPVNLVSVENLCTVIWTPNPPEGASNCSLWYFHFSGDKDKKIAPETRHSE 83
QY 61 EVPLNERICLVGSGCSTNSEDNPSILVEKICISPPGDPESAVTELOQIWHNLSYMKCSW 120
DB 84 EVPLNERICLVGSGCSTNSEDNPSILVEKICISPPGDPESAVTELOQIWHNLSYMKCTW 143
QY 121 LPRNTSPDNTYLYYHRSLEKIHQENIFREGYFCGSDLTAKVDSSFEQHSVQIMV 180
DB 144 LPRNTSPDNTYLYYHRSLEKIHQENIFREGYFCGSDLTAKVDSSFEQHSVQIMV 202
QY 181 KDNAGKIPSNIVPLTSRVKPDPPHINKLSFHNDDLYVQWENPQNFISRCIFYEVEVNN 240
DB 203 KDNAGKIPSNIVPLTSRVKPDPPHINKLSFQNGNLYVQWKNPQNFISRCILSYQVEVNN 262
QY 241 SQTETHNVFYVQEAACENPEPERNVENTSCFMPVPGVLPDNTLVIRVKTNKLCEYDDKL 300
DB 263 TQAKTHDIFYVEEAKQNSSEFEGNLEGMICFMPVPGVLPDNTLVIRVKTNKLCEYDDKL 322
QY 301 WSNWSQMSIGKRNSTLYI 320
DB 323 WSNWSQMSIGKRNSTLYI 342

RESULT 9
Q87597_BOVIN
ID Q87597_BOVIN PRELIMINARY; PRT; 349 AA.
AC Q87597;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin-13 receptor alpha-1 chain (fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20080132; PubMed=10614495; DOI=10.1016/S0165-2427(99)00117-8;
RA Trigona W.L., Brown W.C., Estes D.M.;

RT "Functional implications for signaling via the IL4R/IL13R complex on
RT bovine cells";
RL Vet. Immunol. Immunopathol. 72:73-79(1999).
DR EMBL; AF074402; AAC98147.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytkn recept B/G.
DR InterPro; IPR003532; Hemtptnrecept_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor.
KW Receptor; Transmembrane.
SQ SEQUENCE 1 1
FT NON_TER 349 349
FT SEQUENCE 349 AA; 3664 MW; D61A4C918B1940A6 CRC64;
Query Match 82.0%; Score 1444; DB 2; Length 349;
Best Local Similarity 84.0%; Pred. No. 3.4e-105;
Matches 262; Conservative 15; Mismatches 35; Indels 0; Gaps 0;
QY 9 VTNLSVSVENLCTVIWTPNPEGASSNCSLWYFSGDKQDKKIAPIETRRSI 68
DB 1 VTNLSVSVENLCTVIWTPNPEGASSNCSLWYFSGDKQDKKIAPIETRRSI 60
QY 69 CLQVGSQCSSTNESEKPSILVEKICSPPEGDPESAATVTELOCIWHNLSYMKCSWLPGRNTSP 128
DB 61 CLQVGSQCSSTNESEKPSILVEKICSPPEGDPESAATVTELOCIWHNLSYMKCSWLPGRNASP 120
QY 129 DTYNTLYWHRSLLEKIHCQENIFREGQYFGCSFDLTVKVDSSFEQHSVQIMVKDNAGKIK 188
DB 121 DPNVILYWHNSLGLKIQENFYREGQHIACSFNLTAKVVDSSFEQHSVQIMVKDNAGKIS 180
QY 189 PSNIVPLTSRVKDPDPHINKLSFHNDDLYVQWENPQNFISRCIFYEVEVNSQITHNV 248
DB 181 PSNIVPLTSRVKDPDPHINKLSFHNDDLYVQWENPQNFISRCIFYEVEVNSQITHNV 240
QY 249 FYVQEAACENPEPERNVENTSCFWVPGVLPDLTNTVIRVTKNKLCEYDDKLSNWSQEM 308
DB 241 FYVQEAACQNTFEGNLEGITCFWVPGVLPDLTNTVIRVTKNKLCEYDDKLSNWSQAM 300
QY 309 SICKKRNSTLYI 320
DB 301 SIGQKANQTFYI 312
RESULT 10
Q9UDY5 HUMAN
ID Q9UDY5_HUMAN PRELIMINARY; PRT; 279 AA.
AC Q9UDY5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Interleukin-13 receptor soluble form (interleukin 13 receptor, alpha
1).
DE Names=IL13RAL; ORFNames=RPL3-12804.2-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wada M., Hisano T., Kuwano M.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lawlor S.;
RL SUBMITTED (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -I- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -I- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).

DR EMBL; U81380; AAD00511.2; -; mRNA.
DR EMBL; AL391280; CA141409.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytkn recept B/G.
DR InterPro; IPR003532; Hemtptnrecept_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 279 AA; 31659 MW; E74141FE9F8E9EBB CRC64;
Query Match 78.8%; Score 1387; DB 2; Length 279;
Best Local Similarity 99.6%; Pred. No. 7.6e-101;
Matches 251; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 APTETQPPVTNLSVSVENLCTVIWTPNPEGASSNCSLWYFSGDKQDKKIAPIETRRSI 60
DB 27 APTETQPPVTNLSVSVENLCTVIWTPNPEGASSNCSLWYFSGDKQDKKIAPIETRRSI 86
QY 61 EYPLNERICLVGSQCSSTNESEKPSILVEKICSPPEGDPESAATVTELOCIWHNLSYMKCSW 120
DB 87 EYPLNERICLVGSQCSSTNESEKPSILVEKICSPPEGDPESAATVTELOCIWHNLSYMKCSW 146
QY 121 LPRGNTSPDNTYLYWHRSLLEKIHCQENIFREGQYFGCSFDLTVKVDSSFEQHSVQIMV 180
DB 147 LPRGNTSPDNTYLYWHRSLLEKIHCQENIFREGQYFGCSFDLTVKVDSSFEQHSVQIMV 206
QY 181 KDNAGKIKPSFNIVPLTSRVKDPDPHINKLSFHNDDLYVQWENPQNFISRCIFYEVEVNN 240
DB 207 KDNAGKIKPSFNIVPLTSRVKDPDPHINKLSFHNDDLYVQWENPQNFISRCIFYEVEVNN 266
QY 241 SQTETHNVFYVQ 252
DB 267 SQTETHNVFYVR 278
RESULT 11
IL13RI_MOUSE
ID IL13RI_MOUSE STANDARD; PRT; 424 AA.
AC Q09030; Q7TTT27;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-
13RA-1) (interleukin-13 binding protein) (NR4).
DE Name=IL13ral; Synonyms=il13r, il13ra;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=96133964; PubMed=8552669; DOI=10.1073/pnas.93.1.497;
RA Hilton D.J., Zhang J.-G., Metcalf D., Alexander W.S., Nicola N.A.,
RA Willson T.A.;
RT "Cloning and characterization of a binding subunit of the interleukin
13 receptor that is also a component of the interleukin 4 receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 93:497-501(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=FVB/N; TISSUE=Brain, and Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grumwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Binds IL13 with a low affinity. Together with IL4R-alpha
CC can form a functional receptor for IL13. Also serves as an
CC alternate accessory protein to the common cytokine receptor gamma
CC chain for IL4 signaling, but cannot replace the function of gamma
CC C in allowing enhanced IL2 binding activity (By similarity).
CC -1- SUBUNIT: Interleukin 13 receptor is a complex of IL4R, IL13R1,
CC and possibly other components (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Spleen, liver, thymus, heart, lung, kidney,
CC testis, stomach, brain, skin, and colon; but not skeletal muscle.
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding.
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation.
CC -1- SIMILARITY: Belongs to the type I cytokine receptor family. Type 5
CC subfamily.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL: S80963; AB50695.1; -; mRNA.
CC EMBL: BC052425; AAHS2425.2; -; mRNA.
CC EMBL: BC059939; AAHS9939.1; -; mRNA.
CC Ensembl: ENSMUSG00000017057; Mus musculus.
CC MGI: MGI:105052; IL13ral.
CC GO: GO:0005615; C:extracellular space; TAS.
CC GO: GO:0016021; C:integral to membrane; TAS.
CC InterPro: IPR002996; Cytokn_recept_B/G.
CC InterPro: IPR003532; Hemtpnrecept_F2.
CC PROSITE: PS01356; HEMATOPO REC S_F2; 1.
CC Glycoprotein; Receptor; Signal; Transmembrane.
CC SIGNAL 1 25 Potential.
CC CHAIN 26 424 Interleukin-13 receptor alpha-1 chain.
CC TOPO_DOM 26 340 Extracellular (Potential).
CC TRANSMEM 341 364 Potential.
CC TOPO_DOM 365 424 Cytoplasmic (Potential).
CC MOTIF 324 328 WSXWS motif.
CC MOTIF 371 379 Box 1 motif.
CC CARBOHYD 35 35 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 59 59 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 103 103 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 136 136 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 262 262 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 338 338 N-linked (GlcNAc...) (Potential).
CC DISULFID 44 93 Potential.
CC DISULFID 132 142 By similarity.
CC DISULFID 171 183 By similarity.
CC SEQUENCE 424 AA; 48402 MW; EB8330A0DC82C9f9 CRC64;
Query Match 74.7%; Score 1314.5; DB 1; Length 424;
Best Local Similarity 74.6%; Pred. No. 6.5e-95;
Matches 238; Conservative 35; Mismatches 45; Indels 1; Gaps 1;
QY 1 APTETQPPVNLVSVENLCTVIWNPPEGASSNLSLWYFSGDKQDKKIAPTRRSI 60
Db 25 AATEVQPPVNLVSVENLCTVIWNPPEGASSNLSLWYFSGDKQDKKIAPTRHKE 84
QY 61 EYPLNERICLQVGSQCSTNESEKPSILVEKICSPPEGDPESAVTELQCIWHLNLSYMKCSW 120

Db 85 ELPLDEKICLQVGSQCSTNESEKPSILVEKICSPPEGDPESAVTELQCIWHLNLSYMKCSW 144
QY 121 LPRGNTSPDNTYLYWHRSLKIHOCENIFREGQVFGCSFDLTWKVDSFEQHSQIWMV 180
Db 145 LPRGNTSPDNTYLYWHRSLKIHOCENIFREGQVFGCSFDLTWKVDSFEQHSQIWMV 203
QY 181 KDNAGIKPFSNFTVPLTSRVKPPPHIKNLSPHNDLLYQWENPQNPISCLFYEVEVNN 240
Db 204 KDNAGIKPFSNFTVPLTSRVKPPPHIKNLSPHNDLLYQWENPQNPISCLFYEVEVNN 263
QY 241 SQTETNNVVFQRAKCNPEPFRNVENTSCFMVPGVLPDTLNTVTRVTKNLCYEDDKL 300
Db 264 TQTDREHILLEVEDKQNSSEDRNMGTSQFQLPGVLADAVYTRVRVTKNLCYEDDKL 323
QY 301 WSNWSQMSIGKKNSTLY 319
Db 324 WSDWSEAQSIGKQNSSTLY 342
RESULT 12
Q8C1Z3_MOUSE
ID Q8C1Z3_MOUSE PRELIMINARY; PRT; 424 AA.
AC Q8C1Z3;
DC 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus embryo RCB-0549 Cle-H3 CDNA, RIKEN full-length enriched
DE library, clone:G430044106 product:Interleukin 13 receptor, alpha 1,
DE full insert sequence.
GN Name=Il13ral;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Embryo;
RC MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Embryo;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikola I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
[3]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Embryo;
RC The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of


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Db 25 AATEVQPPVTNLSVSVENLCTIWTWSPPEGASPNCSLRYFSHFDDQQDKKIAPETRKKEL 84
Qy 61 EVPLNERICLVQVGSQCSTNSESKEPSILVEKICISPPGDPDESATVTELOCIWHNLSYMKCSW 120
Db 87 PLNEKICLVQVGSQCSTNSESKEPSILVEKICISPPRGRSESATVTELOCTWHNLSYMKCSWLP 146
Qy 123 GRNTSPDNTYTLYYHRSLEKIHQCENIHREGQYFGCSFDLTVKYDSSPEOHSVQIMVKD 182
Db 147 GKNTSPDNTYTLYYWSSLSKSLQCENIHREGQIHGCSFKLTKV-ESNYEHHNIQIMVKD 205
Qy 183 NAGKIKPSPNIVPLTSRVKPPDPHIIKNLSFHNDDLYVQWENPQNFISRCIFYEVEVNSQ 242
Db 206 NAGKIRPSYKIVGFTSNVKEGPHIKHLFLKNGALFQWKNPQNFSSRCLSYEVEVNSTQ 265
Qy 243 TETH--NVFVQAEAKENPFEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLCEYEDDKL 300
Db 266 TDSYNSNSLEVEDKQNSBFDNRNMEGASCFSIPGVLANVTYTVRVVQTNKLCFDDNDL 325
Qy 301 WSNWSQEMSGKKRNSTLY 319
Db 324 WSDWSEAOISIGKEPNSTFY 342
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RESULT 15

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Q8VHC2_RAT
ID Q8VHC2_RAT PRELIMINARY; PRT; 426 AA.
AC Q8VHC2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE IL-13 receptor alpha 1.
GN Name=il13ral;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Fisher F344;
RC MEDLINE=21458304; PubMed=11573960; DOI=10.1006/bbrc.2001.5682;
RA Pierrot C., Beniguel L., Begue A., Khalife J.;
RT "Expression of a functional IL-13Ralpha1 by rat B cells.";
RL Biochem. Biophys. Res. Commun. 287:969-976(2001).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity)
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
CC EMBL; AY044251; AAK94870.1; -; mRNA.
DR PIR; JC7773; JC7773.
DR Ensembl; ENSRNOG00000013170; Rattus norvegicus.
DR RGD; 628741; Il13ral.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytokn_recept_B/G.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003532; Hemtptnrecept_F2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 426 AA; 48510 MW; 08BPE0E31D9D3C47 CRC64;
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Query Match 72.4%; Score 1274.5; DB 2; Length 426;
Best Local Similarity 72.4%; Pred. No. 9.1e-92;
Matches 231; Conservative 39; Mismatches 46; Indels 3; Gaps 2;
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Db 27 TEVQPPVTNLSVSVENLCTIWTWSPPEGASPNCSLRYFSHFDDQQDKKIAPETRKKEL 86
Qy 63 PLNERICLVQVGSQCSTNSESKEPSILVEKICISPPGDPDESATVTELOCIWHNLSYMKCSWLP 122
Db 87 PLNEKICLVQVGSQCSTNSESKEPSILVEKICISPPRGRSESATVTELOCTWHNLSYMKCSWLP 146
Qy 123 GRNTSPDNTYTLYYHRSLEKIHQCENIHREGQYFGCSFDLTVKYDSSPEOHSVQIMVKD 182
Db 147 GKNTSPDNTYTLYYWSSLSKSLQCENIHREGQIHGCSFKLTKV-ESNYEHHNIQIMVKD 205
Qy 183 NAGKIKPSPNIVPLTSRVKPPDPHIIKNLSFHNDDLYVQWENPQNFISRCIFYEVEVNSQ 242
Db 206 NAGKIRPSYKIVGFTSNVKEGPHIKHLFLKNGALFQWKNPQNFSSRCLSYEVEVNSTQ 265
Qy 243 TETH--NVFVQAEAKENPFEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLCEYEDDKL 300
Db 266 TDSYNSNSLEVEDKQNSBFDNRNMEGASCFSIPGVLANVTYTVRVVQTNKLCFDDNDL 325
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Job time : 112.316 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 22:06:20 ; Search time 26.5039 Seconds
(without alignments)
998.200 Million cell updates/sec

Title: US-10-036-568A-4_COPY_26_345

Perfect score: 1760

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pdp.*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pdp.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pdp.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pdp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1760	100.0	426	2	US-09-688-286D-4
2	1760	100.0	427	2	US-08-969-125-9
3	1760	100.0	427	2	US-09-545-002-9
4	1760	100.0	427	2	US-09-943-016-6094
5	1745	99.1	322	2	US-09-825-561A-82
6	1745	99.1	784	2	US-09-313-942-30
7	1745	99.1	784	2	US-10-282-162-30
8	1745	99.1	793	2	US-09-313-942-32
9	1745	99.1	793	2	US-10-282-162-32
10	1478	84.0	405	2	US-09-828-995B-50
11	1314.5	74.7	424	2	US-09-688-286D-2
12	1265	71.9	233	2	US-09-949-016-8550
13	296	16.8	318	2	US-09-828-995B-69
14	296	16.8	365	2	US-09-828-995B-66
15	296	16.8	386	2	US-09-828-995B-61
16	296	16.8	561	2	US-09-828-995B-72
17	296	16.8	561	2	US-09-828-995B-81
18	296	16.8	563	2	US-09-828-995B-78
19	296	16.8	565	2	US-09-828-995B-75
20	284	16.1	317	2	US-09-825-561A-84
21	284	16.1	380	1	US-08-609-572-4
22	284	16.1	380	2	US-08-841-751-4
23	284	16.1	380	2	US-08-846-340-4
24	284	16.1	380	2	US-08-846-344-4
25	284	16.1	380	2	US-09-301-808-4
26	281	16.0	398	1	US-07-757-390-6
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29	281	16.0	398	1	US-08-939-727-6	Sequence 6, Appli
30	281	16.0	415	1	US-07-757-390-5	Sequence 5, Appli
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33	281	16.0	415	1	US-08-939-727-5	Sequence 5, Appli
34	281	16.0	415	2	US-09-886-319A-23	Sequence 23, Appli
35	278	15.8	383	1	US-08-609-572-2	Sequence 2, Appli
36	278	15.8	383	2	US-08-841-751-2	Sequence 2, Appli
37	278	15.8	383	2	US-08-846-340-2	Sequence 2, Appli
38	278	15.8	383	2	US-08-846-344-2	Sequence 2, Appli
39	277	15.7	335	2	US-09-301-808-2	Sequence 2, Appli
40	277	15.7	335	1	US-07-947-130-3	Sequence 3, Appli
41	277	15.7	335	1	US-08-421-822-3	Sequence 3, Appli
42	277	15.7	335	1	US-08-421-823-3	Sequence 3, Appli
43	272	15.5	255	2	US-09-828-995B-58	Sequence 58, Appli
44	260	14.8	315	1	US-07-757-390-8	Sequence 8, Appli
45	260	14.8	315	1	US-08-442-282-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-688-286D-4
; Sequence 4, Application US/09688286D
; Patent No. 6911530
; GENERAL INFORMATION:
; APPLICANT: Willson, Tracey
; APPLICANT: Nicola, Nicos
; APPLICANT: Hilton, Douglas
; APPLICANT: Metcalf, Donald
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: A novel haemopoietin receptor and genetic sequences encoding same
; FILE REFERENCE: 23199-215
; CURRENT APPLICATION NUMBER: US/09/688,286D
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: AU PN6135
; PRIOR FILING DATE: 1995-10-23
; PRIOR APPLICATION NUMBER: AU PN7276
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: AU PP2208
; PRIOR FILING DATE: 1996-09-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 426
; TYPE: PRT
; ORGANISM: human
US-09-688-286D-4

Query Match 100.0%; Score 1760; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 5.1e-173;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	APTETQPPVTNLSVSNLCVIWTNPPGASNCSLWYFSHFGDKQDKKIAPETRSI	60
Db	26	APTETQPPVTNLSVSNLCVIWTNPPGASNCSLWYFSHFGDKQDKKIAPETRSI	85
Qy	61	EVPLNERICLVGSCSTNESEKPSILVEKICISPPGDPESAVTELCIWNLSYMKCSW	120
Db	86	EVPLNERICLVGSCSTNESEKPSILVEKICISPPGDPESAVTELCIWNLSYMKCSW	145
Qy	121	LPGRNTSPDNTYLYWHSLEKIHQCENIFREGQYFCSDTLTKVKKSSFEQHSVQIMV	180
Db	146	LPGRNTSPDNTYLYWHSLEKIHQCENIFREGQYFCSDTLTKVKKSSFEQHSVQIMV	205
Qy	191	KONAGIKPSNIVPLTSRVKPPPHIKNLSFHNDLVVQWENPNQFISRCILFYEVVNN	240
Db	206	KONAGIKPSNIVPLTSRVKPPPHIKNLSFHNDLVVQWENPNQFISRCILFYEVVNN	265
Qy	241	SQTEHNVFYVQEAECENPEFERNVENTSCFMPGVGLDTLNTVIRVKTNKLCEYDDKL	300

Db 266 SQTEHNVFVQEA KCENPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKL CYEDDKL 325

Qy 301 WSNWSQEMSIGKRNSTLYI 320
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Db 326 WSNWSQEMSIGKRNSTLYI 345
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RESULT 2

US-08-969-125-9
; Sequence 9, Application US/08969125B
; Patent No. 6143871
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, JEAN-YVES
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,125B
; FILING DATE: 12-No. 6143871-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9625899.1
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 427 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-969-125-9

Query Match 100.0%; Score 1760; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 5.1e-173;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTEPTOPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFHFHFGDKQDKKIAPETRRI 60
|||||

Db 27 APTEPTOPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFHFHFGDKQDKKIAPETRRI 86
|||||

Qy 61 EVPLNERICLVQGSQCSTNESEKPSILVEKCI SPPEGD PESAVTELCIWHNLSYMKCSW 120
|||||

Db 87 EVPLNERICLVQGSQCSTNESEKPSILVEKCI SPPEGD PESAVTELCIWHNLSYMKCSW 146
|||||

Qy 121 LPGRNTSPDNTYLYYWHRSLEKIHQCE NIFREGQYFGCSFDLT VKVDSFEGHSVQIMV 180
|||||

Db 147 LPGRNTSPDNTYLYYWHRSLEKIHQCE NIFREGQYFGCSFDLT VKVDSFEGHSVQIMV 206
|||||

Qy 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCIFYEVEVNN 240
|||||

Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCIFYEVEVNN 266
|||||

Qy 241 SQTEHNVFVQEA KCENPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKL CYEDDKL 300
|||||

Db 267 SQTEHNVFVQEA KCENPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKL CYEDDKL 326

Qy 301 WSNWSQEMSIGKRNSTLYI 320
|||||

Db 327 WSNWSQEMSIGKRNSTLYI 346
|||||

RESULT 3

US-09-545-002-9
; Sequence 9, Application US/09545002
; Patent No. 6743604
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, JEAN-YVES
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/545,002
; FILING DATE: 12-No. 6743604-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,125
; FILING DATE: 12-No. 6743604-1997
; APPLICATION NUMBER: GB 9625899.1
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 427 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-545-002-9

Query Match 100.0%; Score 1760; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 5.1e-173;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTEPTOPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFHFHFGDKQDKKIAPETRRI 60
|||||

Db 27 APTEPTOPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFHFHFGDKQDKKIAPETRRI 86
|||||

Qy 61 EVPLNERICLVQGSQCSTNESEKPSILVEKCI SPPEGD PESAVTELCIWHNLSYMKCSW 120
|||||

Db 87 EVPLNERICLVQGSQCSTNESEKPSILVEKCI SPPEGD PESAVTELCIWHNLSYMKCSW 146
|||||

Qy 121 LPGRNTSPDNTYLYYWHRSLEKIHQCE NIFREGQYFGCSFDLT VKVDSFEGHSVQIMV 180
|||||

Db 147 LPGRNTSPDNTYLYYWHRSLEKIHQCE NIFREGQYFGCSFDLT VKVDSFEGHSVQIMV 206
|||||

Qy 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCIFYEVEVNN 240
|||||

Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCIFYEVEVNN 266
|||||


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Qy 241 SQTETHNVFVQAEKCNPEFERNVENTSCFMPVGVLPDTLNTRIRVKTNKLCEYDDKL 300
Db 267 SQTETHNVFVQAEKCNPEFERNVENTSCFMPVGVLPDTLNTRIRVKTNKLCEYDDKL 326
Qy 301 WSNWSQEMSIGKKNSTLYI 320
Db 327 WSNWSQEMSIGKKNSTLYI 346

RESULT 4
US-09-949-016-6094
; Sequence 6094, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6094
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6094

Query Match 100.0%; Score 1760; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 5.1e-173;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFHFSGDKODKKIAPETRRSI 60
Db 27 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFHFSGDKODKKIAPETRRSI 86
Qy 61 EVPLNERICLVGSCSTNESEKPSILVEKICISPPGDPESAVTELOQCIWHLNLSYMKCSW 120
Db 87 EVPLNERICLVGSCSTNESEKPSILVEKICISPPGDPESAVTELOQCIWHLNLSYMKCSW 146
Qy 121 LPGRNTSPDNTLYYHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFQHSVQIMV 180
Db 147 LPGRNTSPDNTLYYHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFQHSVQIMV 206
Qy 181 KDNAGKIKPSFNIPLTSRVKPDPPHINKNLSFHNDLLVQWENPQNFISRCILFYEVVNN 240
Db 207 KDNAGKIKPSFNIPLTSRVKPDPPHINKNLSFHNDLLVQWENPQNFISRCILFYEVVNN 266
Qy 241 SQTETHNVFVQAEKCNPEFERNVENTSCFMPVGVLPDTLNTRIRVKTNKLCEYDDKL 300
Db 267 SQTETHNVFVQAEKCNPEFERNVENTSCFMPVGVLPDTLNTRIRVKTNKLCEYDDKL 326
Qy 301 WSNWSQEMSIGKKNSTLYI 320
Db 327 WSNWSQEMSIGKKNSTLYI 346

RESULT 5
US-09-825-561A-82
; Sequence 82, Application US/09825561A
; Patent No. 677539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. 6777539ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
```

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; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-825-561A-82

Query Match 99.1%; Score 1745; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 1.2e-171;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFHFSGDKODKKIAPETRRSI 60
Db 6 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFHFSGDKODKKIAPETRRSI 65
Qy 61 EVPLNERICLVGSCSTNESEKPSILVEKICISPPGDPESAVTELOQCIWHLNLSYMKCSW 120
Db 66 EVPLNERICLVGSCSTNESEKPSILVEKICISPPGDPESAVTELOQCIWHLNLSYMKCSW 125
Qy 121 LPGRNTSPDNTLYYHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFQHSVQIMV 180
Db 126 LPGRNTSPDNTLYYHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFQHSVQIMV 185
Qy 181 KDNAGKIKPSFNIPLTSRVKPDPPHINKNLSFHNDLLVQWENPQNFISRCILFYEVVNN 240
Db 186 KDNAGKIKPSFNIPLTSRVKPDPPHINKNLSFHNDLLVQWENPQNFISRCILFYEVVNN 245
Qy 241 SQTETHNVFVQAEKCNPEFERNVENTSCFMPVGVLPDTLNTRIRVKTNKLCEYDDKL 300
Db 246 SQTETHNVFVQAEKCNPEFERNVENTSCFMPVGVLPDTLNTRIRVKTNKLCEYDDKL 305
Qy 301 WSNWSQEMSIGKKNST 317
Db 306 WSNWSQEMSIGKKNST 322

RESULT 6
US-09-313-942-30
; Sequence 30, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-313-942-30

Query Match 99.1%; Score 1745; DB 2; Length 784;
Best Local Similarity 100.0%; Pred. No. 4.5e-171;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; SEQ ID NO 32					
; LENGTH: 793					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
US-10-282-162-32					
Query Match 99.1%; Score 1745; DB 2; Length 793;					
Best Local Similarity 100.0%; Pred. No. 4.6e-171; Indels 0; Gaps 0;					
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	APTETOPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSGHFGDKDCKKIAPETRRSI	60		
DB	27	APTETOPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSGHFGDKDCKKIAPETRRSI	86		
QY	61	EVLPLNERICLVGSCQTNESEKPSILVEKCISPPGDPESAVTELOCIIWHNLSYMKCSW	120		
DB	87	EVLPLNERICLVGSCQTNESEKPSILVEKCISPPGDPESAVTELOCIIWHNLSYMKCSW	146		
QY	121	LPGRNTSPDTNYTLYYWHRSLLEKIHOCENIFREGQYFGCSFDLTAKVDSSFEQHSVQIMV	180		
DB	147	LPGRNTSPDTNYTLYYWHRSLLEKIHOCENIFREGQYFGCSFDLTAKVDSSFEQHSVQIMV	206		
QY	181	KDNAGIKKPSFNIVPLTSRVKPDPPHIKNLSFHNDLLVYOWENPQNFSRCLFYEEVNN	240		
DB	207	KDNAGIKKPSFNIVPLTSRVKPDPPHIKNLSFHNDLLVYOWENPQNFSRCLFYEEVNN	266		
QY	241	SOTETHNVFYQEAACENPEFRNVENTSCPMVPGVLPDTLTVTVRIRVKTNKLCYEDDKL	300		
DB	267	SOTETHNVFYQEAACENPEFRNVENTSCPMVPGVLPDTLTVTVRIRVKTNKLCYEDDKL	326		
QY	301	WSNWSQMSIGKKRNST	317		
DB	327	WSNWSQMSIGKKRNST	343		
RESULT 10					
US-09-828-995B-50					
; Sequence 50, Application US/09828995B					
; Patent No. 6703360					
; GENERAL INFORMATION:					
; APPLICANT: Heeka Corporation					
; APPLICANT: McCall, Catherine A.					
; APPLICANT: Tang, Liang A.					
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANIN					
; FILE REFERENCE: AL-7					
; CURRENT APPLICATION NUMBER: US/09/828,995B					
; CURRENT FILING DATE: 2001-04-09					
; PRIOR APPLICATION NUMBER: 60/195,874					
; PRIOR FILING DATE: 2000-04-07					
; PRIOR APPLICATION NUMBER: 60/195,659					
; PRIOR FILING DATE: 2000-04-07					
; NUMBER OF SEQ ID NOS: 104					
; SOFTWARE: PatentIn version 3.1					
; SEQ ID NO 50					
; LENGTH: 405					
; TYPE: PRT					
; ORGANISM: Canis familiaris					
US-09-828-995B-50					
Query Match 84.0%; Score 1478; DB 2; Length 405;					
Best Local Similarity 83.4%; Pred. No. 6.3e-144;					
Matches 267; Conservative 22; Mismatches 31; Indels 0; Gaps 0;					
QY	1	APTETOPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSGHFGDKDCKKIAPETRRSI	60		
DB	5	APTETOPPVTNLSVSVENLCTVIWTWNPPEGASPNECTLYRFHFNDKQDKKIAPETRHSK	64		
QY	61	EVLPLNERICLVGSCQTNESEKPSILVEKCISPPGDPESAVTELOCIIWHNLSYMKCSW	120		
DB	65	EVLPLNERICLVGSCQTNESDNPSILVEKCTPPPEGDPSAVTELOCVVHNLSYMKCTW	124		
QY	121	LPGRNTSPDTNYTLYYWHRSLLEKIHOCENIFREGQYFGCSFDLTAKVDSSFEQHSVQIMV	180		

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Db      125  LPGRNTSPDNTYTYLTYWHSLSGLKILQCEDIYRSEQHIGCSFALTNLKDSSPEQHSVQIMV 181
Qy      181  KDNAGKIKPSFNTVPLTSRVKPPPHIKNI6LSFNDDLYVQWENPQNFISRCCLFYEV2EVNN 240
Db      185  KDNARKIRPSFNIVPLTSHVKPDPDPHHIKRL6PFQNGNLVYQWKNPQNFYSRCLSYQVE2VNN 244
Qy      241  SQTETHNVFYQEAACENPESFERNVENTSCFMVPGVL6PDLTNTVRI2RVKTNKLCYEDDKL 300
Db      245  SQTETNDIFYVEBAKQNSFEGNLEGTICFMVPGVL6PDLTNTVRI2RVKTNKLCYEDDKL 304
Qy      301  WSNWSQEMSIGKKRNSTLYI 320
Db      305  WSNWSQMSIGENTDPTFYI 324

RESULT 11
US-09-688-286D-2
; Sequence 2, Application US/09688286D
; Patent No. 6911530
; GENERAL INFORMATION:
; APPLICANT: Willson, Tracey
; APPLICANT: Nicola , Nicos
; APPLICANT: Hilton, Douglas
; APPLICANT: Metcalf, Donald
; APPLICANT: Zhang , Jian
; TITLE OF INVENTION: A novel haemopoietin receptor and genetic sequences enc
; FILE REFERENCE: 23199-215
; CURRENT APPLICATION NUMBER: US/09/688,286D
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: AU P66135
; PRIOR FILING DATE: 1995-10-23
; PRIOR APPLICATION NUMBER: AU P67276
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: AU P62208
; PRIOR FILING DATE: 1996-09-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-688-286D-2

Query Match 74.7%; Score 1314.5; DB 2; Length 424;
Best Local Similarity 74.6%; Pred. No. 5.2e-127;
Matches 238; Conservative 35; Mismatches 45; Indels 1; Gaps 1

Qy      1  APTETQPPVNLVSVENLCTVI6TWNPPEGASSNC6SLWYF6SHFGDKODKKIAPETR6RSI 60
Db      25  AATEVQPPVNLVSVENLCTVI6TWNSPEGASPNCTLI6RYF6SHFDQDDKKIAPETH6RKE 84
Qy      61  EVLNERICLVGQCSQNSSEKPSILY6KEKICISPEGDP6PE6SAVTE6LQCI6WHNLSYMKCSW 120
Db      85  ELPDEKICLVGQCSQNSSEKPSPL6VK6ICISPEGDP6PE6SAVTE6LKCI6WHNLSYMKCSW 144
Qy      121  LPGRNTSPDNTYTYLTYWHSLSGLKILQCEDIYRSEQHIGCSFALTNLKDSSPEQHSVQIMV 180
Db      145  LPGRNTSPDTHYTYLTYWHSLSGLKILQCEDIYRSEQHIGCSFALTNLKDSSPEQHSVQIMV 203
Qy      181  KDNAGKIKPSFNIVPLTSRVKPPPHIKNI6LSFNDDLYVQWENPQNFISRCCLFYEV2EVNN 240
Db      204  KDNARKIRPSCKIVSLTSYVVKPDPDPHHIKHL6LKNGALLVQWKNPQNFYSRCLTYEV2VNN 263
Qy      241  SQTETHNVFYQEAACENPESFERNVENTSCFMVPGVL6PDLTNTVRI2RVKTNKLCYEDDKL 300
Db      264  TQTRHNTILEVEDKQNSDRNMEGISC6FQ6LPGLADAVYTVRVKTNKLCYEDDKL 323
Qy      301  WSNWSQEMSIGKKRNSTLYI 319
Db      324  WSDWSEAQSIGKEQNSTFY 342

RESULT 12

```

RESULT 12

US-09-949-016-8550
; Sequence 8550, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8550
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8550

Query Match 71.9%; Score 1265; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 2.7e-122; Indels 0; Gaps 0;
Matches 231; Conservative 0; Mismatches 0;
QY 51 KIAPTRRSIEVPLNERICLQVGSQCSTNESEKPSILVEKCISSPPGDPESAVTELQCIW 110
DB 1 KIAPTRRSIEVPLNERICLQVGSQCSTNESEKPSILVEKCISSPPGDPESAVTELQCIW 60
QY 111 HNL SYMKCSWLPGRNTSPDNTYLYWHRSLKIHOCENIFREGQYFGCSFDTLTKVDSS 170
DB 61 HNL SYMKCSWLPGRNTSPDNTYLYWHRSLKIHOCENIFREGQYFGCSFDTLTKVDSS 120
QY 171 FEQHSQIWMKDNAGIKPSFNVLTSRVKPPPHIKNLSFNDDLYVQWENPQNFISR 230
DB 121 FEQHSQIWMKDNAGIKPSFNVLTSRVKPPPHIKNLSFNDDLYVQWENPQNFISR 180
QY 231 CLFYEVVNNQSOTETHNVFYVQAKCENPEFERNVENTSCFMVPGVLPDTL 281
DB 181 CLFYEVVNNQSOTETHNVFYVQAKCENPEFERNVENTSCFMVPGVLPDTL 231

RESULT 13
US-09-828-995B-69
; Sequence 69, Application US/09828995B
; Patent No. 6703360
; GENERAL INFORMATION:
; APPLICANT: Heeka Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IgG AND CANINE IL-13 R
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/09/828,995B
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-828-995B-69

Query Match 16.8%; Score 296; DB 2; Length 318;
Best Local Similarity 26.9%; Pred. No. 5.1e-22;
Matches 83; Conservative 52; Mismatches 115; Indels 58; Gaps 15;

QY 26 WNPPL--EGASSNCSLWY---FSHFGDKQDKIAP-----ETRRSIEVPLNERICLQ 71
DB 32 WQPLFPDPNFKECTIEYELKYRNIDSENWKTITKNLHYKDGFDLNGKEAKINTLL--- 88
QY 72 VGSQCSTNESEKPSILVEKCI-SPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDT 130
DB 89 -PAQC-TNGSEVRSSWAETTYWTSPOGNETRIQDMDCVYVNWQYLVCWSKPGMVHFD 146
QY 131 NYTLYWHRSLKIHOCENIFR-EGQYFGCSFDTLTKVDSSFEQHSQIWMKDNAGIKP 189
DB 147 NYQLFYWYEGLDHSAECTDYIKVNGKNMGRFPY--LESSDYKDFYICVNGSSESQFIRP 204
QY 190 SFNIVPLTSRVKPPPHIKNLSFHN--DDLVOVENPQNFISRCLFYEVVNNQSOTETH 245
DB 205 SYFIFQLQNIWVMPDPDYLSTLVKNSSEINLKNMFKGPIPAKCFIYEIEFTEDGTWVT 264
QY 246 HNVFYVQAKCENPEFERNVENTS-----CFMVPGLVLPDTLNTVIRVKTNNKLCYEDDK 299
DB 265 TTV-----ENEIQITRTSNESQKLCFLV-----RSKVNIYC-SDDG 299
QY 300 LWSNWSQ 307
DB 300 IWSNSDE 307

RESULT 14
US-09-828-995B-66
; Sequence 66, Application US/09828995B
; Patent No. 6703360
; GENERAL INFORMATION:
; APPLICANT: Heeka Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IgG AND CANINE IL-13 R
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/09/828,995B
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-828-995B-66

Query Match 16.8%; Score 296; DB 2; Length 365;
Best Local Similarity 26.9%; Pred. No. 6.3e-22;
Matches 83; Conservative 52; Mismatches 115; Indels 58; Gaps 15;

QY 26 WNPPL--EGASSNCSLWY---FSHFGDKQDKIAP-----ETRRSIEVPLNERICLQ 71
DB 31 WQPLFPDPNFKECTIEYELKYRNIDSENWKTITKNLHYKDGFDLNGKEAKINTLL--- 87
QY 72 VGSQCSTNESEKPSILVEKCI-SPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDT 130
DB 88 -PAQC-TNGSEVRSSWAETTYWTSPOGNETRIQDMDCVYVNWQYLVCWSKPGMVHFD 145
QY 131 NYTLYWHRSLKIHOCENIFR-EGQYFGCSFDTLTKVDSSFEQHSQIWMKDNAGIKP 189
DB 146 NYQLFYWYEGLDHSAECTDYIKVNGKNMGRFPY--LESSDYKDFYICVNGSSESQFIRP 203
QY 190 SFNIVPLTSRVKPPPHIKNLSFHN--DDLVOVENPQNFISRCLFYEVVNNQSOTETH 245
DB 204 SYFIFQLQNIWVMPDPDYLSTLVKNSSEINLKNMFKGPIPAKCFIYEIEFTEDGTWVT 263
QY 246 HNVFYVQAKCENPEFERNVENTS-----CFMVPGLVLPDTLNTVIRVKTNNKLCYEDDK 299
DB 264 TTV-----ENEIQITRTSNESQKLCFLV-----RSKVNIYC-SDDG 298

Qy 300 LWSNWSOE 307
Db 299 IWSEWSDE 306

RESULT 15
US-09-828-995B-61
; Sequence 61, Application US/09828995B
; Patent No. 6703360
; GENERAL INFORMATION:
; APPLICANT: Heskia Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IgG AND CANINE IL-13 R
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/09/828,995B
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-828-995B-61

Query Match 16.8%; Score 296; DB 2; Length 386;
Best Local Similarity 26.9%; Pred. No. 6.8e-22;
Matches 83; Conservative 52; Mismatches 115; Indels 58; Gaps 15;

Qy 26 WNP-EGASNCSLWY---FSHFGDKODKXIAP-----ETRRSIEVPLNERICLQ 71
Db 52 WOPLPDPNFKECTIEYELKYRNIDSENWKTIIITKNLHYKDGFDLNGKIEAKINTLL--- 108

Qy 72 VGSQCSTNESKPSILVEKCI-SPEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDT 130
Db 109 -PAQC-TNGSEVRSSWAETTYTSPQGNRETKIQDMDCVYINWQYLVCSWPKGMGVHFD 166

Qy 131 NYTLYYHRSLEKTHOCNIFR-EGQYFGCSFDLTKKVDSSEFQHSVQIMVKDNAGKIKP 189
Db 167 NYQLFYWTEGLDHSABCTDYIKVNGKMGCRFPY--LESSDYKDFYICVNGSSSQIRP 224

Qy 190 SFNIVPLTSRVKPPDPPIHKNLSFHN-DDLYVQWENPQNF-SRCLFYEVVNNSQTE--T 245
Db 225 SYFIFQLQNIWKMPDYLSTLVKNSBINLKNWPKGPIPAKCFIYBIEFTEDGTTWVT 284

Qy 246 HNVFYQAKCENPEFRNVENTS-----CFWVPGVLPTINTVIRVTKNKLCEYDDK 299
Db 285 TTV-----ENEIQTITNSQKLCFLV-----RSKVNYYC-SDDG 319

Qy 300 LWSNWSOE 307
Db 320 IWSEWSDE 327

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 22:28:54 ; Search time 86.7655 Seconds
(without alignments)
1540.998 Million cell updates/sec

Title: US-10-036-568A-4_COPY_26_345

Perfect score: 1760

Sequence: 1 APTETQPPVTNLSVSVENLCTVIWNPPEGSSNCSLWYFHFSGDKQDKKIAPETRRSI 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1760	100.0	427	4	US-10-671-697-9 Sequence 9, Appli
2	1760	100.0	427	5	US-10-850-270-4 Sequence 4, Appli
3	1760	100.0	427	6	US-11-067-251-3 Sequence 3, Appli
4	1745	99.1	322	3	US-09-823-561A-82 Sequence 82, Appl
5	1745	99.1	322	5	US-10-872-087-82 Sequence 82, Appl
6	1745	99.1	664	5	US-10-850-270-10 Sequence 10, Appl
7	1745	99.1	776	3	US-09-935-868-36 Sequence 36, Appl
8	1745	99.1	780	3	US-09-935-868-34 Sequence 34, Appl
9	1745	99.1	784	3	US-09-313-942-30 Sequence 30, Appl
10	1745	99.1	784	3	US-09-935-868-30 Sequence 30, Appl
11	1745	99.1	784	4	US-10-287-035-30 Sequence 30, Appl
12	1745	99.1	784	4	US-10-282-162-30 Sequence 30, Appl
13	1745	99.1	784	6	US-11-134-114-30 Sequence 30, Appl
14	1745	99.1	793	3	US-09-313-942-32 Sequence 32, Appl
15	1745	99.1	793	3	US-09-935-868-32 Sequence 32, Appl
16	1745	99.1	793	4	US-10-287-035-32 Sequence 32, Appl
17	1745	99.1	793	4	US-10-282-162-32 Sequence 32, Appl
18	1745	99.1	793	6	US-11-134-114-32 Sequence 32, Appl
19	1742	99.0	426	4	US-10-036-568-4 Sequence 4, Appli
20	1736	98.6	776	3	US-09-935-868-44 Sequence 44, Appl
21	1736	98.6	776	6	US-11-067-251-8 Sequence 8, Appli
22	1736	98.6	776	6	US-11-067-251-10 Sequence 10, Appl
23	1736	98.6	776	6	US-11-067-251-12 Sequence 12, Appl
24	1736	98.6	776	6	US-11-067-251-14 Sequence 14, Appl
25	1736	98.6	776	6	US-11-067-251-16 Sequence 16, Appl
26	1736	98.6	778	3	US-09-935-868-46 Sequence 46, Appl
27	1736	98.6	778	4	US-10-287-035-46 Sequence 46, Appl

28	1736	98.6	778	4	US-10-287-035-60	Sequence 60, Appl
29	1736	98.6	780	3	US-09-935-868-42	Sequence 42, Appl
30	1736	98.6	782	3	US-09-935-868-48	Sequence 48, Appl
31	1735	98.6	776	3	US-09-935-868-40	Sequence 40, Appl
32	1735	98.6	778	3	US-09-935-868-50	Sequence 50, Appl
33	1735	98.6	778	4	US-10-287-035-50	Sequence 50, Appl
34	1735	98.6	778	4	US-10-287-035-56	Sequence 56, Appl
35	1735	98.6	780	3	US-09-935-868-38	Sequence 38, Appl
36	1735	98.6	782	3	US-09-935-868-52	Sequence 52, Appl
37	1731.5	98.4	780	4	US-10-287-035-34	Sequence 34, Appl
38	1729	98.2	776	4	US-10-287-035-40	Sequence 40, Appl
39	1722.5	97.9	780	4	US-10-287-035-42	Sequence 42, Appl
40	1722.5	97.9	782	4	US-10-287-035-48	Sequence 48, Appl
41	1722.5	97.9	782	4	US-10-287-035-54	Sequence 54, Appl
42	1721.5	97.8	780	4	US-10-287-035-38	Sequence 38, Appl
43	1721.5	97.8	782	4	US-10-287-035-52	Sequence 52, Appl
44	1721.5	97.8	782	4	US-10-287-035-58	Sequence 58, Appl
45	1720	97.7	776	4	US-10-287-035-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-10-671-697-9
; Sequence 9, Application US/10671697
; Publication No. US20040043921A1
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, JEAN-YVES
; GAUCHAT, JEAN-FRANCOIS
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/671,697
; FILING DATE: 29-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/545,002
; FILING DATE: 06-APR-2000
; APPLICATION NUMBER: US 08/969,125
; FILING DATE: 12-NOV-1997
; APPLICATION NUMBER: GB 9625899.1
; FILING DATE: 13-DEC-1996
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 427 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-671-697-9

Query Match 100.0%; Score 1760; DB 4; Length 427;
Best Local Similarity 100.0%; Pred. No. 2.2e-148;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APTETQPPVTNLSVSVENLCTVIWNPPEGSSNCSLWYFHFSGDKQDKKIAPETRRSI 60
DB 27 APTETQPPVTNLSVSVENLCTVIWNPPEGSSNCSLWYFHFSGDKQDKKIAPETRRSI 86
QY 61 EVPLNERICLVGSCQSTNESKPSILVEKCISSPEGDPESAVTELQCIWHNLSYMKCSW 120

Db 87 EVPLNERICLVGSCSTNESEKPSILVEKICSPPEGDPESAVTELCIWHNLSYMKCSW 146
Qy 121 LPRGNTSPDNTYLYWHRSLKIHQCNIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
Db 147 LPRGNTSPDNTYLYWHRSLKIHQCNIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 206
Qy 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSPHNDLLYQWENPQNFISRCLFYEVVNN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSPHNDLLYQWENPQNFISRCLFYEVVNN 266
Qy 241 SQTEHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLCEYDDKL 300
Db 267 SQTEHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLCEYDDKL 326
Qy 301 WSNWSQEMSIGKKNSTLYI 320
Db 327 WSNWSQEMSIGKKNSTLYI 346

RESULT 2

US-10-850-270-4
; Sequence 4, Application US/10850270
; Publication No. US20050058645A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd (for all States except the US)
; APPLICANT: Dunlop, Felicity (US only)
; APPLICANT: Baca, Manuel (US only)
; APPLICANT: Nash, Andrew (US only)
; APPLICANT: Fabri, Louis (US only)
; TITLE OF INVENTION: Novel peptides
; FILE REFERENCE: 12175890/EJH
; CURRENT APPLICATION NUMBER: US/10/850,270
; PRIOR FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: AU P81301
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: AU 2003900437
; PRIOR FILING DATE: 2003-02-03
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 427
; TYPE: PRT
; ORGANISM: human
US-10-850-270-4

Query Match 100.0%; Score 1760; DB 5; Length 427;
Best Local Similarity 100.0%; Pred. No. 2.2e-148;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 APTETQPPVTNLVSVENLCTVIWTPNPPGASNCSLWYFSGDKQKKIAPETRRSI 60
Db 27 APTETQPPVTNLVSVENLCTVIWTPNPPGASNCSLWYFSGDKQKKIAPETRRSI 86
Qy 61 EVPLNERICLVGSCSTNESEKPSILVEKICSPPEGDPESAVTELCIWHNLSYMKCSW 120
Db 87 EVPLNERICLVGSCSTNESEKPSILVEKICSPPEGDPESAVTELCIWHNLSYMKCSW 146
Qy 121 LPRGNTSPDNTYLYWHRSLKIHQCNIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
Db 147 LPRGNTSPDNTYLYWHRSLKIHQCNIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 206
Qy 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSPHNDLLYQWENPQNFISRCLFYEVVNN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSPHNDLLYQWENPQNFISRCLFYEVVNN 266
Qy 241 SQTEHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLCEYDDKL 300
Db 267 SQTEHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLCEYDDKL 326
Qy 301 WSNWSQEMSIGKKNSTLYI 320
Db 327 WSNWSQEMSIGKKNSTLYI 346

RESULT 3

US-11-067-251-3
; Sequence 3, Application US/11067251
; Publication No. US20050191730A1
; GENERAL INFORMATION:
; APPLICANT: Karow, Margaret
; APPLICANT: Fairhurst, Jeanette
; TITLE OF INVENTION: IL-4/IL-13 Specific Polypeptides and Therapeutic Uses Thereof
; FILE REFERENCE: 2020A
; CURRENT APPLICATION NUMBER: US/11/067,251
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 60/548,541
; PRIOR FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: 60/602,139
; PRIOR FILING DATE: 2004-08-17
; PRIOR APPLICATION NUMBER: 60/628,343
; PRIOR FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-067-251-3

Query Match 100.0%; Score 1760; DB 6; Length 427;
Best Local Similarity 100.0%; Pred. No. 2.2e-148;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 APTETQPPVTNLVSVENLCTVIWTPNPPGASNCSLWYFSGDKQKKIAPETRRSI 60
Db 27 APTETQPPVTNLVSVENLCTVIWTPNPPGASNCSLWYFSGDKQKKIAPETRRSI 86
Qy 61 EVPLNERICLVGSCSTNESEKPSILVEKICSPPEGDPESAVTELCIWHNLSYMKCSW 120
Db 87 EVPLNERICLVGSCSTNESEKPSILVEKICSPPEGDPESAVTELCIWHNLSYMKCSW 146
Qy 121 LPRGNTSPDNTYLYWHRSLKIHQCNIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
Db 147 LPRGNTSPDNTYLYWHRSLKIHQCNIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 206
Qy 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSPHNDLLYQWENPQNFISRCLFYEVVNN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSPHNDLLYQWENPQNFISRCLFYEVVNN 266
Qy 241 SQTEHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLCEYDDKL 300
Db 267 SQTEHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLCEYDDKL 326
Qy 301 WSNWSQEMSIGKKNSTLYI 320
Db 327 WSNWSQEMSIGKKNSTLYI 346

RESULT 4

US-09-825-561A-82
; Sequence 82, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677A1ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05

		PRIOR APPLICATION NUMBER: US 60/222,121			
		PRIOR FILING DATE: 2000-07-28			
		NUMBER OF SEQ ID NOS: 86			
		SOFTWARE: FastSeq for Windows Version 3.0			
		SEQ ID NO 82			
		LENGTH: 322			
		TYPE: PRT			
		ORGANISM: Homo sapiens			
		US-09-825-561A-82			
		Query Match 99.1%; Score 1745; DB 3; Length 322;			
		Best Local Similarity 100.0%; Pred. No. 3.3e-147;			
		Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	APTETQPPVTNLVSVENLCTVIWTPNPPGASNCSLWYFSGDKQDKKIAPETR	RSI	60	
Db	6	APTETQPPVTNLVSVENLCTVIWTPNPPGASNCSLWYFSGDKQDKKIAPETR	RSI	65	
Qy	61	EVPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW		120	
Db	66	EVPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW		125	
Qy	121	LPGRNTSPDNTYTLYYWHSLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV		180	
Db	126	LPGRNTSPDNTYTLYYWHSLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV		185	
Qy	181	KDNAGIKKPSFNIIVPLTSRVKPDPPHINKNLSFHNDLLYQWENPQNFISRCLFYEV	VNN	240	
Db	186	KDNAGIKKPSFNIIVPLTSRVKPDPPHINKNLSFHNDLLYQWENPQNFISRCLFYEV	VNN	245	
Qy	241	SQTETHNVFYVQEAKECNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKL	CYEDDKL	300	
Db	246	SQTETHNVFYVQEAKECNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKL	CYEDDKL	305	
Qy	301	WSNWSQEMSIGKKRNST	317		
Db	306	WSNWSQEMSIGKKRNST	322		
		RESULT 6			
		US-10-850-270-10			
		; Sequence 10, Application US/10850270			
		; Publication No. US2005058645A1			
		; GENERAL INFORMATION:			
		; APPLICANT: AMRAD Operations Pty Ltd (for all States except the US)			
		; APPLICANT: Dunlop, Felicity (US only)			
		; APPLICANT: Baca, Manuel (US only)			
		; APPLICANT: Nash, Andrew (US only)			
		; APPLICANT: Fabri, Louis (US only)			
		; TITLE OF INVENTION: Novel peptides			
		; FILE REFERENCE: 12175890/EH			
		; CURRENT APPLICATION NUMBER: US/10/850,270			
		; CURRENT FILING DATE: 2004-05-20			
		; PRIOR APPLICATION NUMBER: AU P81301			
		; PRIOR FILING DATE: 2002-03-22			
		; PRIOR APPLICATION NUMBER: AU 2003900437			
		; PRIOR FILING DATE: 2003-02-03			
		; NUMBER OF SEQ ID NOS: 28			
		; SOFTWARE: PatentIn version 3.1			
		; SEQ ID NO 10			
		; LENGTH: 664			
		; TYPE: PRT			
		; ORGANISM: human			
		US-10-850-270-10			
		Query Match 99.1%; Score 1745; DB 5; Length 664;			
		Best Local Similarity 100.0%; Pred. No. 8.6e-147;			
		Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	APTETQPPVTNLVSVENLCTVIWTPNPPGASNCSLWYFSGDKQDKKIAPETR	RSI	60	
Db	45	APTETQPPVTNLVSVENLCTVIWTPNPPGASNCSLWYFSGDKQDKKIAPETR	RSI	104	
Qy	61	EVPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW		120	
Db	105	EVPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW		164	
Qy	121	LPGRNTSPDNTYTLYYWHSLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV		180	
Db	165	LPGRNTSPDNTYTLYYWHSLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV		224	
Qy	181	KDNAGIKKPSFNIIVPLTSRVKPDPPHINKNLSFHNDLLYQWENPQNFISRCLFYEV	VNN	240	
Db	225	KDNAGIKKPSFNIIVPLTSRVKPDPPHINKNLSFHNDLLYQWENPQNFISRCLFYEV	VNN	284	
Qy	241	SQTETHNVFYVQEAKECNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKL	CYEDDKL	300	
Db	285	SQTETHNVFYVQEAKECNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKL	CYEDDKL	344	

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QY 301 WSNWSQEMSIGKCRNST 317
Db 345 WSNWSQEMSIGKCRNST 361
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RESULT 7
US-09-935-868-36
; Sequence 36, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-36

Query Match 99.1%; Score 1745; DB 3; Length 776;
Best Local Similarity 100.0%; Pred. No. 1.1e-146;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTETOPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFHFHFGDKQDKKIAPETRRSI 60
Db 232 APTETOPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFHFHFGDKQDKKIAPETRRSI 291
|||||

QY 61 EVELNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 120
Db 292 EVELNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 351
|||||

QY 121 LPGRNTSPDNTNYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
Db 352 LPGRNTSPDNTNYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 411
|||||

QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNDDLYVOWENPQNFISRCLFYEVVNN 240
Db 412 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNDDLYVOWENPQNFISRCLFYEVVNN 471
|||||

QY 241 SQTETHNVFYVQEAACENPFERNVENTSCFMVPGVLPDTLNTVIRVKTNKL CYEDDKL 300
Db 472 SQTETHNVFYVQEAACENPFERNVENTSCFMVPGVLPDTLNTVIRVKTNKL CYEDDKL 531
|||||

QY 301 WSNWSQEMSIGKCRNST 317
Db 532 WSNWSQEMSIGKCRNST 548
|||||

RESULT 8
US-09-935-868-34
; Sequence 34, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 780
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-34

Query Match 99.1%; Score 1745; DB 3; Length 784;
Best Local Similarity 100.0%; Pred. No. 1.1e-146;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTETOPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFHFHFGDKQDKKIAPETRRSI 60
Db 239 APTETOPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFHFHFGDKQDKKIAPETRRSI 298
|||||

QY 61 EVELNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 120
Db 299 EVELNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 358
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QY 121 LPGRNTSPDNTNYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
Db 359 LPGRNTSPDNTNYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 418
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QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNDDLYVOWENPQNFISRCLFYEVVNN 240
Db 419 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNDDLYVOWENPQNFISRCLFYEVVNN 478
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Qy 241 SQTETHNVFYVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYDDKL 300
Db 479 SQTETHNVFYVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYDDKL 538
Qy 301 WSNWSQEMSGKKNST 317
Db 539 WSNWSQEMSGKKNST 555
RESULT 10
US-10-935-868-30
; Sequence 30, Application US/09935868
; Publication No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-935-868-30
Query Match 99.1%; Score 1745; DB 3; Length 784;
Best Local Similarity 100.0%; Pred. No. 1.1e-146; Indels 0; Gaps 0;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 239 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFHFGDKODKXIAPETRRI 298
Qy 61 EVPLNERICLQVGSQCSTNESEKPSILVEKICISPEGDPESAVTELOCIWHNLSYMKCSW 120
Db 299 EVPLNERICLQVGSQCSTNESEKPSILVEKICISPEGDPESAVTELOCIWHNLSYMKCSW 358
Qy 121 LPGRNTSPDNTYLYYHRSLEKIHOCENIFREGQYFGCSFDLTAKVDSSFEQHSVQIMV 180
Db 359 LPGRNTSPDNTYLYYHRSLEKIHOCENIFREGQYFGCSFDLTAKVDSSFEQHSVQIMV 418
Qy 181 KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLLYVQWENPQNFISRCLFYEVENVN 240
Db 419 KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLLYVQWENPQNFISRCLFYEVENVN 478
Qy 241 SQTETHNVFYVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYDDKL 300
Db 479 SQTETHNVFYVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYDDKL 538
Qy 301 WSNWSQEMSGKKNST 317
Db 539 WSNWSQEMSGKKNST 555
RESULT 11
US-10-287-035-30
; Sequence 30, Application US/10287035
; Publication No. US20030104567A1
; GENERAL INFORMATION:
; APPLICANT: Neil Stahl and George D. Yancopoulos
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203DA
; CURRENT APPLICATION NUMBER: US/10/287,035
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: USSN 09/935,868
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: USSN 09/787,835
; PRIOR FILING DATE: 2001-03-22

; PRIOR APPLICATION NUMBER: USSN 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-035-30
Query Match 99.1%; Score 1745; DB 4; Length 784;
Best Local Similarity 100.0%; Pred. No. 1.1e-146; Indels 0; Gaps 0;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFHFGDKODKXIAPETRRI 60
Db 239 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFHFGDKODKXIAPETRRI 298
Qy 61 EVPLNERICLQVGSQCSTNESEKPSILVEKICISPEGDPESAVTELOCIWHNLSYMKCSW 120
Db 299 EVPLNERICLQVGSQCSTNESEKPSILVEKICISPEGDPESAVTELOCIWHNLSYMKCSW 358
Qy 121 LPGRNTSPDNTYLYYHRSLEKIHOCENIFREGQYFGCSFDLTAKVDSSFEQHSVQIMV 180
Db 359 LPGRNTSPDNTYLYYHRSLEKIHOCENIFREGQYFGCSFDLTAKVDSSFEQHSVQIMV 418
Qy 181 KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLLYVQWENPQNFISRCLFYEVENVN 240
Db 419 KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLLYVQWENPQNFISRCLFYEVENVN 478
Qy 241 SQTETHNVFYVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYDDKL 300
Db 479 SQTETHNVFYVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYDDKL 538
Qy 301 WSNWSQEMSGKKNST 317
Db 539 WSNWSQEMSGKKNST 555
RESULT 12
US-10-282-162-30
; Sequence 30, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-30
Query Match 99.1%; Score 1745; DB 4; Length 784;
Best Local Similarity 100.0%; Pred. No. 1.1e-146; Indels 0; Gaps 0;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFHFGDKODKXIAPETRRI 60
Db 239 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFHFGDKODKXIAPETRRI 298

QY 61 EVPLNERICLVGSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120
DB 299 EVPLNERICLVGSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 358
QY 121 LPRGNTSPDNTYLYYWHRSLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
DB 359 LPRGNTSPDNTYLYYWHRSLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 418
QY 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFNHDDLQVQWENPQNFISRCLFYEVVNN 240
DB 419 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFNHDDLQVQWENPQNFISRCLFYEVVNN 478
QY 241 SQTETHNVFYQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVTRIRVTKNKLCEYEDDKL 300
DB 479 SQTETHNVFYQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVTRIRVTKNKLCEYEDDKL 538
QY 301 WSNWSQEMSIGKKNST 317
DB 539 WSNWSQEMSIGKKNST 555
RESULT 13
US-11-134-114-30
; Sequence 30, Application US/11134114
; Publication No. US2005022033A1
; GENERAL INFORMATION:
; APPLICANT: Stahl, Neil
; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: Receptor Based Antagonists and Methods of Making and Using
; FILE REFERENCE: 203CI
; CURRENT APPLICATION NUMBER: US/11/134,114
; PRIOR FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-114-30

Query Match 99.1%; Score 1745; DB 6; Length 784;
Best Local Similarity 100.0%; Pred. No. 1.1e-146;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 EVPLNERICLVGSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120
DB 299 EVPLNERICLVGSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 358
QY 121 LPRGNTSPDNTYLYYWHRSLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
DB 359 LPRGNTSPDNTYLYYWHRSLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 418
QY 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFNHDDLQVQWENPQNFISRCLFYEVVNN 240
DB 419 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFNHDDLQVQWENPQNFISRCLFYEVVNN 478
QY 241 SQTETHNVFYQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVTRIRVTKNKLCEYEDDKL 300

DB 479 SQTETHNVFYQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVTRIRVTKNKLCEYEDDKL 538
QY 301 WSNWSQEMSIGKKNST 317
DB 539 WSNWSQEMSIGKKNST 555
RESULT 14
US-09-313-942-32
; Sequence 32, Application US/09313942
; Publication No. US20020012962A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-32

Query Match 99.1%; Score 1745; DB 3; Length 793;
Best Local Similarity 100.0%; Pred. No. 1.1e-146;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 EVPLNERICLVGSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120
DB 87 EVPLNERICLVGSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 146
QY 121 LPRGNTSPDNTYLYYWHRSLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
DB 147 LPRGNTSPDNTYLYYWHRSLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 206
QY 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFNHDDLQVQWENPQNFISRCLFYEVVNN 240
DB 207 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFNHDDLQVQWENPQNFISRCLFYEVVNN 266
QY 241 SQTETHNVFYQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVTRIRVTKNKLCEYEDDKL 300
DB 267 SQTETHNVFYQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVTRIRVTKNKLCEYEDDKL 326
QY 301 WSNWSQEMSIGKKNST 317
DB 327 WSNWSQEMSIGKKNST 343

RESULT 15
US-09-935-868-32
; Sequence 32, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-32

Query Match      99.1%; Score 1745; DB 3; Length 793;
Best Local Similarity 100.0%; Pred. No. 11e-146;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   |||||||
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Db   |||||||
Qy 61  EVPLNERICLVGSGQCSSTNESEKPSILVEKCI SPPEGDPESAVTELOCIWHNLSYMKCSW 120
Db   |||||||
Qy 87  EVPLNERICLVGSGQCSSTNESEKPSILVEKCI SPPEGDPESAVTELOCIWHNLSYMKCSW 146
Db   |||||||
Qy 121 LPGRNTSPDNTYTLYYWHSLEKIHQENIFREGQYFGCSFDLTKVXDSFQHSVQIMV 180
Db   |||||||
Qy 147 LPGRNTSPDNTYTLYYWHSLEKIHQENIFREGQYFGCSFDLTKVXDSFQHSVQIMV 206
Db   |||||||
Qy 181 KDNAGKIKPSPFNIVPLTSRVKPDPPHIKNLSFHNDLLYVQWENPQNFISRCIFYEVEVNN 240
Db   |||||||
Qy 207 KDNAGKIKPSPFNIVPLTSRVKPDPPHIKNLSFHNDLLYVQWENPQNFISRCIFYEVEVNN 266
Db   |||||||
Qy 241 SQTETHNVFYVQEAACENPEPERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKL 300
Db   |||||||
Qy 267 SQTETHNVFYVQEAACENPEPERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKL 326
Db   |||||||
Qy 301 WSNWSQEMSIGKKNST 317
Db   |||||||
Qy 327 WSNWSQEMSIGKKNST 343
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 22:29:50 ; Search time 6.97472 Seconds
(without alignments)
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Title: US-10-036-568A-4_COPY_26_345

Perfect score: 1760

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/1/pubpaa/US08 NEW PUB.pap.*
2: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pap.*
3: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pap.*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pap.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	1305.5	74.2	424	7	US-11-185-230-6
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4	284	16.1	380	6	US-10-989-313-4
5	284	16.1	380	7	US-11-185-230-2
6	278	15.8	383	6	US-10-989-313-2
7	230	13.1	313	7	US-11-193-512-106
8	230	13.1	420	7	US-11-185-230-5
9	181.5	10.3	341	6	US-10-511-722-21
10	181.5	10.3	357	6	US-10-511-722-20
11	181.5	10.3	369	7	US-11-105-268-60
12	178.5	10.1	411	7	US-11-075-351-47
13	168.5	9.6	329	6	US-10-995-561-694
14	168.5	9.6	646	6	US-10-995-561-695
15	168.5	9.6	708	6	US-10-636-320-2
16	168.5	9.6	918	6	US-10-995-561-696
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19	144	8.2	903	7	US-11-124-367A-450
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21	110.5	6.3	825	7	US-11-124-367A-469
22	110.5	6.3	852	7	US-11-104-923A-5
23	107	6.1	631	6	US-10-813-646-22
24	102.5	5.8	1905	6	US-10-877-346-44
25	101.5	5.8	896	7	US-11-192-219-3
26	101.5	5.8	898	7	US-11-166-730-3
27	101.5	5.8	923	7	US-11-192-219-4
28	101.5	5.8	1165	7	US-11-192-219-2
29	100.5	5.7	2214	7	US-11-080-991-94
30	95.5	5.4	1433	7	US-11-094-519A-40
31	93	5.3	783	7	US-11-192-219-7
32	91.5	5.2	551	7	US-11-022-289-7
33	91.5	5.2	836	6	US-10-821-234-1559
34	90	5.1	979	6	US-10-636-320-6
35	89	5.1	1452	6	US-10-821-234-1102
36	88.5	5.0	557	7	US-11-022-289-2
37	88.5	5.0	557	7	US-11-022-289-5
38	88	5.0	489	6	US-10-835-475-11
39	88	5.0	514	6	US-10-835-475-2
40	87.5	5.0	984	7	US-11-113-424-60
41	87	4.9	1254	6	US-10-528-031-47
42	86	4.9	1706	7	US-11-052-554A-176
43	85.5	4.9	557	7	US-11-022-289-4
44	85.5	4.9	557	7	US-11-022-289-6
45	85.5	4.9	1259	6	US-10-995-561-625

ALIGNMENTS

RESULT 1

US-11-185-230-4
; Sequence 4, Application US/11185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio

; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185.230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 427
; TYPE: PRT 3
; ORGANISM: Homo sapiens
; FEATURE:
US-11-185-230-4

Query Match	100.0%;	Score 1760;	DB 7;	Length 427;
Best Local Similarity	100.0%;	Pred. No. 5e-153;		
Matches 320;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	APETQPPVTNLSVSVENLCTVITWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI	60	
Db	27	APETQPPVTNLSVSVENLCTVITWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI	86	
QY	61	EVPLNERICLVGSCSTNESEKPSILVEKICISPEGDPESAVTELQCIWHNLSYMKCSW	120	
Db	87	EVPLNERICLVGSCSTNESEKPSILVEKICISPEGDPESAVTELQCIWHNLSYMKCSW	146	
QY	121	LPGRNTSPDTNVTLYYHRSLEKIHQCENIFREGQYFGCSFDLTVKVQDSSFQHSVQIMV	180	
Db	147	LPGRNTSPDTNVTLYYHRSLEKIHQCENIFREGQYFGCSFDLTVKVQDSSFQHSVQIMV	206	
QY	181	KDNAGKIKPSFNIVELTSRVKPDPPHIIKNLSFHNDDLYVQWENPQNFISRCLFYEVVNN	240	
Db	207	KDNAGKIKPSFNIVELTSRVKPDPPHIIKNLSFHNDDLYVQWENPQNFISRCLFYEVVNN	266	
QY	241	SQTETHNFFVQEAECENPEFERNVENTSCFMPVGLPDTLNTVIRVTKNLCYEDDKL	300	
Db	267	SQTETHNFFVQEAECENPEFERNVENTSCFMPVGLPDTLNTVIRVTKNLCYEDDKL	326	

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QY 301 WSNWSQEMSGKKRNSTLYI 320
Db 327 WSNWSQEMSGKKRNSTLYI 346

RESULT 2
US-11-185-230-6
; Sequence 6, Application US/11185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 424
; TYPE: PRT 3
; ORGANISM: Mus musculus
; FEATURE:
US-11-185-230-6

Query Match 74.2%; Score 1305.5; DB 7; Length 424;
Best Local Similarity 74.3%; Pred. No. 1.3e-111;
Matches 237; Conservative 35; Mismatches 46; Indels 1; Gaps 1;

QY 1 APTETQPPVTLNLSVSNLCTVIWTWNPPEGASNSCLWYFHFHGDQDKKIAPETRRSI 60
Db 25 AATEVQPPVTLNLSVSNLCTVIWTWNPPEGASPNCTLRYFHFHGDQDKKIAPETHRKE 84

QY 61 EVPLNERICLOVGSQCSTNESEKPSILVEKCIIPPEDGPESAVTELOCIWHNLSYMKCSW 120
Db 85 ELPLDERIKICLOVGSQCSANSEKPSPLVKKCIIPPEDGPESAVTELOCIWHNLSYMKCSW 144

QY 121 LPGRNTSPDNTLYYWHRSLEKIHQCNIFREGQYFGCSFDLTQVKDSSFEQHSVQIMV 180
Db 145 LPGRNTSPDNTLYYWHRSLEKSRQCNIFREGQHIACSKFKTKV-EPSEFHQNVQIMV 203

QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLIVQWENPQNFIISRCLFYEVVN 240
Db 204 KDNAGKIRPCKIVSLTSYVKPPPHIKHLLKNGALLVQWKNPQNPFRSRLTYEVVN 263

QY 241 SQETHNVFVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVTRVTKNLCYEDDKL 300
Db 264 TOTDRHILEVEEDKCNSESDRNMEGTSCFQLPGVLADAVYTVRVVTKNLCYEDDKL 323

QY 301 WSNWSQEMSGKKRNSTLYI 319
Db 324 WSDWSEAQSGKQNSTFY 342

RESULT 3
US/11/185
; Sequence 12, Application US/11185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
```

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; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 378
; TYPE: PRT 3
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: variant of SEQ ID NO. 2 in which the sequence VRCVTL is substituted
US/11/185,230-12
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Query Match 16.1%; Score 284; DB 7; Length 378;
Best Local Similarity 28.7%; Pred. No. 1.3e-18;
Matches 88; Conservative 47; Mismatches 116; Indels 56; Gaps 16;

QY 26 WNPPEGAS--SNCSLWYFHFHGDQDKKIAPETRRSI-----EVPLNERICLOVGS 74
Db 53 WQPPLSLDHPKECTVEY-----ELKYRNIGSETWTKIITKNLHYKQDFDLNKGIEAKIHT 107

QY 75 -----QCSTNESEKPSILVEKC--ISPEDGPESAVTELOCIWHNLSYMKCSWLPGRNTSP 128
Db 108 LLPWQC-TNGSEVOSSWAETTYWIS--PQGIPTKVQDMDCVYNNQVLLCSWPKGIGVLL 165

QY 129 DTNYTLYYWHRSLEKIHQCNIFREGQYFGCSFDLTQVKDSSFEQHSVQIMVKDNAGKI 187
Db 166 DTNYNLPYWYEGLDHALQCDVYIKADQGNIGCFPPYLEASD--YKDFYICVNGSSENKPI 223

QY 188 KPSFNIVPLTSRVKPPPHIKNLSFHNDDLIVQWENPQNFI-ISRCLFYEVVNNSQT 243
Db 224 RSSYFTFQLQNIYVKPLPP--VYLTFRESSCEIKLWKSIPGLGPIPARCFDYEIEIREDDT 281

QY 244 ETHNVFVQAEKCNPEFERNVENTS---CFMYPGVLPDTLNTVTRVTKNLCYEDDKL 300
Db 282 T-----LVTATVENSETYTLTKTTNETRQLCFVW-----RSKNIIYC-SDDGI 321

QY 301 WSNWSQEMSGKKRNSTLYI 307
Db 322 WSEWSDK 328
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RESULT 4
US-10-989-313-4
; Sequence 4, Application US/10989313
; Publication No. US20050277126A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lora
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; APPLICANT: Wills-Karp, Marsha
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: Cytokine Receptor Chain
; FILE REFERENCE: GI 5268A
; CURRENT APPLICATION NUMBER: US/10/989,313
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US/09/868,123
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-989-313-4
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Query Match 16.1%; Score 284; DB 6; Length 380;
Best Local Similarity 28.7%; Pred. No. 1.4e-18;
Matches 88; Conservative 47; Mismatches 116; Indels 56; Gaps 16;

QY 26 WNPPEGAS--SNCSLWYFHFHGDQDKKIAPETRRSI-----EVPLNERICLOVGS 74
Db 53 WQPPLSLDHPKECTVEY-----ELKYRNIGSETWTKIITKNLHYKQDFDLNKGIEAKIHT 107
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QY 75 ----OCSTNESEKPSILVEK--ISPPEGDPSAVTELCIWHNLSYMKCSWLPGRNTSP 128
Db 108 LLPWQC-TNGSEVQSSWAETTYWIS-POGIPETKVQDMDCVYINWQYLLCSWKRGIGVLL 165
QY 129 DTNTYLYWHRSLRKIHQC-ENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKI 187
Db 166 DTYNLFWYEGLDHALQCDVDYIKADQGNIGCRFPYLEASD--YKDFYICVNGSSSENKPI 223
QY 188 KPSFNIVPLTSRVKDPDPHIIKNLSFHND---DLVQWENPQNFI-SRCLFYEVENVNSQT 243
Db 224 RSSYFTFQLOQIVKPLPP--VYLTFRESSCEIKLWKSIPGLPIPARCFDYEIREDDT 281
QY 244 ETHNVFYQEAKECENPEPERNVENTS---CFMWPGVLPDLTNTVIRVKTNKLCEYDDKL 300
Db 282 T-----LVTATVENETTYLTKTNTETROLQCFV-----RSKNYIC-SDDGI 321
QY 301 WSNWSOE 307
Db 322 WSEWSDK 328

RESULT 5
US-11-185-230-2
; Sequence 2, Application US/111185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: INV924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-11-185-230-2
Query Match 16.1%; Score 284; DB 7; Length 380;
Best Local Similarity 28.7%; Pred. No. 1.4e-18;
Matches 88; Conservative 47; Mismatches 116; Indels 56; Gaps 16;

QY 26 WNPPEGAS--SNCSLWYFSHFGDKQDKKIAPETRSI-----EVLNERICLQVGS 74
Db 53 WQPLSLDHFKECTVEY-----ELKYRNISETWTKIITKNLHYKDGFDLKNKGIKTIHT 107
QY 75 ----OCSTNESEKPSILVEK--ISPPEGDPSAVTELCIWHNLSYMKCSWLPGRNTSP 128
Db 108 LLPWQC-TNGSEVQSSWAETTYWIS-POGIPETKVQDMDCVYINWQYLLCSWKRGIGVLL 165
QY 129 DTNTYLYWHRSLRKIHQC-ENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKI 187
Db 166 DTYNLFWYEGLDHALQCDVDYIKADQGNIGCRFPYLEASD--YKDFYICVNGSSSENKPI 223
QY 188 KPSFNIVPLTSRVKDPDPHIIKNLSFHND---DLVQWENPQNFI-SRCLFYEVENVNSQT 243
Db 224 RSSYFTFQLOQIVKPLPP--VYLTFRESSCEIKLWKSIPGLPIPARCFDYEIREDDT 281
QY 244 ETHNVFYQEAKECENPEPERNVENTS---CFMWPGVLPDLTNTVIRVKTNKLCEYDDKL 300
Db 282 T-----LVTATVENETTYLTKTNTETROLQCFV-----RSKNYIC-SDDGI 321
QY 301 WSNWSOE 307
Db 322 WSEWSDK 328
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RESULT 6

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US-10-989-313-2
; Sequence 2, Application US/10989313
; Publication No. US20050277126A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lora
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; APPLICANT: Wills-Karp, Marsha
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: Cytokine Receptor Chain
; FILE REFERENCE: GI 5268A
; CURRENT APPLICATION NUMBER: US/10/989,313
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US/09/868,123
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-989-313-2
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Query Match 15.8%; Score 278; DB 6; Length 383;
Best Local Similarity 26.0%; Pred. No. 4.8e-18;
Matches 77; Conservative 47; Mismatches 138; Indels 34; Gaps 11;

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QY 26 WNPP-----EGASSNCSLWYFSHFGDKQDKKIAPETRSIEVPLNE----RICLQVGSQ 75
Db 47 WKPVPVIEKFKGCTLEYELKYRNVDSWSWTKIITRNLIYKDGFDLKNKGIKTIHLSH 106
QY 76 CSTNESEKPSILVEKCISS--PPEGDPSAVTELCIWHNLSYMKCSWLPGRNTSPDTNTYL 134
Db 107 C-TNGSEVQSSWAETTYWIS-POGIPETKVQDMDCVYINWQYLLCSWKRGIGVLL 165
QY 135 YYWHRSLRKIHQCENIFR-EGQYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKI KPSFNI 193
Db 166 FFWYEGLDHALQCADYLQHDENKVGCK--LSNLDSDDYKDFPICVNGSSKLEPIRSSYTV 223
QY 194 VPLTSRVKDPDPHIIKNLSFHND-DLVQWENPQNFI-SRCLFYEVENVNSQTETNVFV 251
Db 224 FQLOQIVKPLPEPFLHISVENSIDIRMKWSTPGGIPPRCYTYEIVIREDDISWESATDK 283
QY 252 QEAKECENPEPERNVENTS--CFMWPGVLPDLTNTVIRVKTNKLCEYDDKLWSNWSOE 307
Db 284 NDMKLK---RANESDLCFFV-----RCKVNIYC-ADDDGIWSEWSEE 322
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RESULT 7

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US-11-193-512-106
; Sequence 106, Application US/111193512
; Publication No. US20050272918A1
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; APPLICANT: FURUYA, Akiko
; APPLICANT: NAKAMURA, Kazuyasu
; APPLICANT: IIDA, Akihiro
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: HANAI, Nobuo
; APPLICANT: TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
```



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; CURRENT APPLICATION NUMBER: US/11/105,268
; CURRENT FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: 60/561,845
; PRIOR FILING DATE: 2004-04-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-268-60

Query Match          10.3%; Score 181.5; DB 7; Length 369;
Best Local Similarity 26.8%; Pred. No. 2.9e-09;
Matches 61; Conservative 39; Mismatches 87; Indels 41; Gaps 12;

QY 105 ELQCIWHNLSYKMCWLPGRNTSPDNTYTLYYWHRSLL--EKIHQCEN-IFREGQYFGCSF 161
DB 59 EVQCFVFNVEYMNCTWNSSEPOF--TNLTLLHYWYKNSDNDKVKQKSHYLFSEBITSGC-- 115

QY 162 DLTKVKDSSPEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPPDPPIHKNLSFH---NDDLY 218
DB 116 QLOKKEIHLYQTFVQL--QDPREPRQATQMLKQLNVLIPWAP--ENLTLLHKLSSQLE 171

QY 219 VQWENPQNFIISRL-----FYEVVNNSSQTEHNVFVQEAACENPFRNVENTSCFMVP 274
DB 172 LNMNN--RFLNHCHLEHLVQYRTDWDHSWT-----EQSDVYRHKFSLP 211

QY 275 GVLPDTLNTRVRKTNKLCYEDDKLWSNWSQEMSIG---KKNRSTLY 319
DB 212 SVDGQKRYTFRVRSRNPCLC-GSAQHWSHSPHIGWSNTSKENPPLF 258

RESULT 12
US-11-075-351-47
; Sequence 47, Application US/11075351
; Publication No. US20050260716A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Margaret D.
; APPLICANT: Fox, Brian A.
; TITLE OF INVENTION: DIMERIC FUSION PROTEINS AND MATERIALS
; TITLE OF INVENTION: AND METHODS FOR PRODUCING THEM
; FILE REFERENCE: 02-16
; CURRENT APPLICATION NUMBER: US/11/075,351
; CURRENT FILING DATE: 2005-03-08
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein
US-11-075-351-47

Query Match          10.1%; Score 178.5; DB 7; Length 411;
Best Local Similarity 26.5%; Pred. No. 6.1e-09;
Matches 60; Conservative 39; Mismatches 86; Indels 41; Gaps 12;

QY 105 ELQCIWHNLSYKMCWLPGRNTSPDNTYTLYYWHRSLL--EKIHQCEN-IFREGQYFGCSF 161
DB 72 EVQCFVFNVEYMNCTWNSSEPOF--TNLTLLHYWYKNSDNDKVKQKSHYLFSEBITSGC-- 128

QY 162 DLTKVKDSSPEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPPDPPIHKNLSFH---NDDLY 218
DB 129 QLOKKEIHLYQTFVQL--QDPREPRQATQMLKQLNVLIPWAP--ENLTLLHKLSSQLE 184

QY 219 VQWENPQNFIISRL-----FYEVVNNSSQTEHNVFVQEAACENPFRNVENTSCFMVP 274
DB 185 LNMNN--RFLNHCHLEHLVQYRTDWDHSWT-----EQSDVYRHKFSLP 224

QY 275 GVLPDTLNTRVRKTNKLCYEDDKLWSNWSQEMSIG---KKNRST 317

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Db 225 SVDGQKRYTFRVRSRNPCLC-GSAQHWSWSHPHGWGNTSKENG 269
 Best Local Similarity 25.3%; Pred. No. 8.6e-08;
 Matches 80; Conservative 45; Mismatches 148; Indels 43; Gaps 16;
 RESULT 13
 US-10-995-561-694
 ; Sequence 694, Application US/10995561
 ; Publication No. US20050272054A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
 ; TITLE OF INVENTION: DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001559
 ; CURRENT FILING DATE: 2004-11-24
 ; CURRENT APPLICATION NUMBER: US/10/995,561
 ; NUMBER OF SEQ ID NOS: 85702
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 694
 ; LENGTH: 329
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-995-561-694
 Query Match 9.6%; Score 168.5; DB 6; Length 329;
 Best Local Similarity 25.3%; Pred. No. 3.8e-08;
 Matches 80; Conservative 45; Mismatches 148; Indels 43; Gaps 16;
 QY 6 QPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFSHFG-DKODKKIAPETRSIEVPL 64
 Db 34 ESPVQLHSNFTTAVCVLKEKMDYFHVNNYIVWKTNHTPTPKQYTIINRTASSVTFTD 93
 QY 65 NERICLVQSGQSTNESEKPSILVEKICIS--PPEGDPESAVTELCIWHNLSYMKCSWLP 122
 Db 94 IASLNLQILCNLTITFQLEQNVYGITIISGLPPE-KPKN----LSCIVNEGKKWRCWDG 148
 QY 123 GRNTSPDNTYTL-YYWHRSLKIHOCENIFREGQVFGCSFDLTVKVQSSFPQHSVQIMVK 181
 Db 149 GRETHLETNFTLKSEW--ATHKFADCK--AKRDTPTCTVDYSTV---YFVNIEVWVEAE 201
 QY 182 DNAGKI-KPSFNIVPLTSRVKDPDPHKNLSFHNDD-----LYQWENPQNFISRCFLYE 235
 Db 202 NALGKVTSDHINFPDPV-YKVKPNPPH--NLSVINSEELSSILKLTWNPSPKSVIILKYN 258
 QY 236 VEVNNSQTETHNVFYVQEAKECNPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKL 295
 Db 259 IQYRTKDASTWS-----QIPP-EDTASTRSFTVQDLKPTTEYVFRIR-----CM 302
 QY 296 EDD--KLMSNWSQEMS 309
 Db 303 KEDGKGYSWDSWEAS 318
 RESULT 14
 US-10-995-561-695
 ; Sequence 695, Application US/10995561
 ; Publication No. US20050272054A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
 ; TITLE OF INVENTION: DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001559
 ; CURRENT FILING DATE: 2004-11-24
 ; CURRENT APPLICATION NUMBER: US/10/995,561
 ; NUMBER OF SEQ ID NOS: 85702
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 695
 ; LENGTH: 646
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-995-561-695
 Query Match 9.6%; Score 168.5; DB 6; Length 646;
 Best Local Similarity 25.3%; Pred. No. 8.6e-08;
 Matches 80; Conservative 45; Mismatches 148; Indels 43; Gaps 16;
 RESULT 15
 US-10-636-320-2
 ; Sequence 2, Application US/10636320
 ; Publication No. US20050260197A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mosley, Bruce
 ; TITLE OF INVENTION: Receptor for Oncostatin M
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Apple 7.1
 ; SOFTWARE: Microsoft Word, Version 5.1a
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/636,320
 ; FILING DATE: 06-Aug-2003
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 10/313,135
 ; FILING DATE: 2002-12-06
 ; APPLICATION NUMBER: US/08/308,881
 ; FILING DATE: 12-SEP-1994
 ; APPLICATION NUMBER: US 08/249,553
 ; FILING DATE: 26-MAY-1994
 ; APPLICATION NUMBER: US/09/058,264
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: US/08/308,881
 ; FILING DATE: 12-SEP-1994
 ; APPLICATION NUMBER: US 08/249,553
 ; FILING DATE: 26-MAY-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seese, Kathryn A.
 ; REGISTRATION NUMBER: 32,172
 ; REFERENCE/DOCKET NUMBER: 2614-A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 587-0430
 ; TELEFAX: (206) 233-0644

```

;
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 708 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-636-320-2

Query Match      9.6%; Score 168.5; DB 6; Length 708;
Best Local Similarity 25.3%; Pred. No. 9.6e-08;
Matches 80; Conservative 45; Mismatches 148; Indels 43; Gaps 16;

Qy 6 QPPVTNLSVSVENLCTVIWTPNPEGASSNSLWYFSHFG-DKQDKKIAPETRRSIEVPL 64
Db 34 ESPVVQLHSNFTAVCVLKEKCMDFHVNANYIVMKNHTIPKEQYTIINRTASSVTFTD 93

Qy 65 NERICLQVGSQCSTNESEKPSILVEKCIS--PREGDPESAATELQCIWHNLSYMKCSWLP 122
Db 94 IASLNIQTNCNLTGQLEQNVYGITIISGLPPE-KPKN-----LSCIVNEGKMKRCWDG 148

Qy 123 GRNTPSDTNYTL-YWHRSLKIHQCENIPEGQYFGCSFDLTKVKDSSPEQHSVQIMVK 181
Db 149 GRETHLETNFTLKSEW--ATHKPADCK--AKBDTPTCTVDYSTV---YFVNIEVWVEAE 201

Qy 182 DNAGKI-KPSFNIYPLTSRVKPDPPHIKNLSFHND-----LYVQWENPONFISRCIFYE 235
Db 202 NALGKVTSDHINFDPV-YKVKPNPPH--NLSVINSEELSLILKLTWTNPSIKSVIILKYN 258

Qy 236 VEVNNSQTETHNVFVQEKACENPEFENVENTSCENVPGVLPDPLNTVIRVKTNKLKY 295
Db 259 IQYRTKDASTWS-----QIPP-EDTASTRSSFTVQDLKPFTEVVRIR-----CM 302

Qy 296 EDD--KLWSNWSQBS 309
Db 303 KEDGKGYSWDSSEAS 318

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Search completed: February 8, 2006, 22:35:24
Job time : 7.97472 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 21:52:58 ; Search time 123.412 Seconds
(without alignments)
1427.670 Million cell updates/sec

Title: US-10-036-568A-4_COPY_26_426
Perfect score: 2172
Sequence: 1 APFETQPPVNLVSVENLC.....QTKETDSVVLIENLKASQ 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A Geneseq 21.*
- 1: Geneseqp1980s.*
 - 2: Geneseqp1990s.*
 - 3: Geneseqp2000s.*
 - 4: Geneseqp2001s.*
 - 5: Geneseqp2002s.*
 - 6: Geneseqp2003as.*
 - 7: Geneseqp2003bs.*
 - 8: Geneseqp2004as.*
 - 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2172	100.0	414	8	Adx97531 Pancreati
2	2172	100.0	426	2	Aaw09822 Human int
3	2172	100.0	427	2	Aaw24973 Human int
4	2172	100.0	427	4	Aab19807 Human int
5	2172	100.0	427	8	Adl171812 Human int
6	2172	100.0	427	8	Adl82843 Human PRO
7	2172	100.0	427	8	Adn04504 Antipsori
8	2172	100.0	427	8	Adn62575 Human int
9	2172	100.0	427	8	Abm82441 Tumour-as
10	2166	99.7	427	8	Adl171813 Human int
11	2165	99.7	427	7	Adf17835 Human IL-
12	2165	99.7	427	8	Adl171814 Human int
13	2159	99.4	427	4	Aab19808 Human int
14	1869	86.0	405	4	Aau69132 Canine in
15	1784.5	82.2	664	7	Adf17841 Chimeric
16	1749.5	80.5	784	3	Aay92207 IL-13/IL-
17	1749.5	80.5	784	7	Abw02180 Human IL-
18	1745	80.3	322	5	Aae13745 Human sol
19	1745	80.3	793	3	Aay92208 IL-13/IL-
20	1745	80.3	793	7	Abw02181 Human IL-
21	1698	78.2	426	2	Aaw09821 Mouse int
22	1688.5	77.7	424	9	Adx97888 Murine IL
23	1536	70.7	286	4	Aab90678 Human DAL
24	942	43.4	177	2	Aaw58987 Homo sapi

ALIGNMENTS

RESULT 1
ADX97531

ID ADX97531 standard; protein; 414 AA.

XX AC ADX97531;
XX AC
DT 21-APR-2005 (first entry)
XX DE Pancreatic cancer associated human protein, SEQ ID 79.
XX KW pancreas tumor; cytostatic.
XX OS Homo sapiens.
XX FN EP1471075-A2.
XX PD 27-OCT-2004.
XX PF 31-MAR-2004; 2004EP-00090124.
XX PR 31-MAR-2003; 2003DB-01015834.

XX PA (HINZ/) HINZMANN B.
XX PA (ROSE/) ROSENTHAL A.
XX PA (PILA/) PILARSKY C.
XX PA (DAHL/) DAHL E.
XX PA (SPEC/) SPECHT T.
XX PA (LICHT/) LICHTNER R.
XX PI Rosenthal A, Pilarisky C, Dahl E, Specht T, Bruemendorf T;
XX PI Lichtner R, Staub E, Roepcke S, Li X;
XX WPI; 2004-768082/76.
XX N-PSDB; ADX97460.

XX PT New nucleic acid differentially expressed in pancreatic tumor tissue, for
XX use as diagnostic agents and in screening for therapeutic agents.
XX PS Claim 2; SEQ ID NO 79; 28pp; German.

XX CC The invention relates to a novel human nucleic acid sequence of the
XX CC pancreas and its encoded protein. The invention further comprises:
XX CC proteins and peptides, preferably isolated that contain a sequence
XX CC encoded by the novel nucleic acid; and methods for diagnosis and
XX CC treatment of pancreatic cancer, using a substance that inhibits or binds
XX CC to the protein or its DNA, including: an antisense oligonucleotide, short
XX CC interfering RNA or ribozyme directed against the pancreatic protein, an

Adp84617 Human bre
Adp84616 Human bre
Adq65618 Novel hum
Aar22212 Sequence
Aar22211 Sequence
Aar22217 Sequence
Adz58697 Mouse IL-
Aau69136 Canine in
Aau69135 Canine in
Aau69138 Canine IL
Aau69141 Canine IL
Aaw36616 Celebus m
Aau69139 Canine IL
Adz58698 Human IL-
Aar25064 Human IL-
Aau69137 Canine IL
Aau69140 Canine IL
Aaw36613 Human Zcy
Aaw35295 Human IL-
Aaw24972 Human int
Aaw33603 Homo sapi

Db	266	SQTETHNVFYQEAKECPENPERNVNTSCFMVPGVLPDTLNTVIRVKTNKLCYEDDKL	325
Qy	301	WSNWSQEMSIGKGRNSTLYITMLLIVPVIVAGAIIVLLVLLKRLKIIIFPPIDPGKIFK	360
Db	326	WSNWSQEMSIGKGRNSTLYITMLLIVPVIVAGAIIVLLVLLKRLKIIIFPPIDPGKIFK	385
Qy	361	EMFGDQNDTLLHWKKYDIYEKQTKETDSVLIENLKASQ	401
Db	386	EMFGDQNDTLLHWKKYDIYEKQTKETDSVLIENLKASQ	426
RESULT 3			
AAW24973			
ID	AAW24973	standard; protein; 427 AA.	
XX	AC	AAW24973;	
XX	DT	22-JUN-1998 (first entry)	
XX	DE	Human interleukin-13 alpha receptor.	
XX	KW	Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13.	
XX	OS	Homo sapiens.	
XX	FN	W09720926-A1.	
XX	PD	12-JUN-1997.	
XX	PF	07-NOV-1996; 96WO-FR001756.	
XX	PR	06-DEC-1995; 95FR-00014424.	
XX	PA	(SNFI) SANOFI SA.	
XX	PI	Caput D, Ferrara P, Laurent P, Vita N;	
XX	DR	WPI; 1997-319773/29.	
XX	DR	N-PSDB; AAT85827.	
PT	New purified human interleukin-13 receptors - and related nucleic acids,		
PT	useful for diagnosis and treatment of inflammation, allergy, etc.		
PS	Claim 8; Page 46-47; 83pp; French.		
CC	This sequence represents interleukin-13 (IL-13) alpha receptor. The		
CC	invention relates to new purified peptides comprising 380 or 427 amino		
CC	acid sequences, which are receptors for interleukin-13 (IL-13); the 380		
CC	and 427 aa proteins are designated IL-13R beta and alpha respectively.		
CC	The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low		
CC	affinity, but acquires high affinity when associated with the IL-4		
CC	receptor. Nucleic acids encoding IL-13R beta and alpha are used as		
CC	diagnostic probes to identify aberrant synthesis or genetic anomalies		
CC	such as loss of heterozygosity and rearrangements, or chromosomal		
CC	anomalies. They are also used for production of recombinant IL-13R beta		
CC	and alpha which can be used as IL-13 antagonists, specifically to		
CC	regulate IL-13-induced responses for treatment of inflammation and		
CC	allergy. IL-13 receptors are also useful as antisense molecules for gene		
CC	therapy (blocking synthesis of IL-13R). Antibodies are used (in standard		
CC	immunoassays) to diagnose diseases associated with abnormal expression of		
CC	IL-13 receptors; when coupled to a toxin also for treatment of		
CC	overproduction of IL-13R. Cells that express IL-13R at the surface are		
CC	used to identify ligands and modulators of IL-13R		
XX	Sequence 427 AA;		
SQ	Query Match 100.0%; Score 2172; DB 2; Length 427;		
	Best Local Similarity 100.0%; Pred. No. 3.3e-201;		
	Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	APTETQPPVTVNLVSVENLCTVIWTVNPPGASSNCSLWYFSHFQDKQDKKIAPETRSI	60
Db	27	APTETQPPVTVNLVSVENLCTVIWTVNPPGASSNCSLWYFSHFQDKQDKKIAPETRSI	86

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DR N-PSDB; AAA88907.
XX Novel polypeptide capable of binding interleukin-13 or interleukin-4
PT useful for treating atopy, atopic dermatitis, allergies, rhinitis,
PT eczema, asthma or AIDS.
XX
PS Claim 2; Fig 1A; 26pp; English.
XX
CC The present sequence is that of a protein capable of binding human
CC interleukin-13 (IL-13) and/or human interleukin-4 (IL-4) in the presence
CC of IL-4 receptor alpha. It was deduced from cDNA (see AAA88907) isolated
CC from a human activated tonsillar cDNA library. This IL-13 receptor alpha-1
CC polypeptide can be used to inhibit IL-13 or IL-4 induced IgE synthesis in
CC B cells, useful in the treatment of diseases in which IgE or Th2
CC differentiation plays a role, e.g. atopy, atopic dermatitis, allergy,
CC rhinitis, eczema, asthma or AIDS. Antibodies raised against the
CC polypeptide are useful for detecting IL-13 and IL-4 receptor or parts of
CC them which have been shed from cells as a result of disease, e.g. cancer,
CC leukaemia, atopy, atopic dermatitis, allergies, rhinitis, eczema, asthma,
CC lupus erythematosus, AIDS, thyroiditis, diabetes, uveitis, dermatitis,
CC psoriasis, urticaria, nephrotic syndrome, inflammatory bowel disease,
CC glomerulonephritis, ulcerative colitis, Crohn's disease, Sjogren's
CC syndrome and toxoplasmosis
XX
SQ Sequence 427 AA;

Query Match      100.0%; Score 2172; DB 4; Length 427;
Best Local Similarity 100.0%; Pred. No. 3.3e-201;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTETOPPVTNLVSVENLCTVIWTWNPPEGASNSCLWYFHFSGDKQDKKIAPETRRSI 60
DB 27 APTETOPPVTNLVSVENLCTVIWTWNPPEGASNSCLWYFHFSGDKQDKKIAPETRRSI 86
QY 61 EVPLNERICLVQSGSQSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 120
DB 87 EVPLNERICLVQSGSQSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 146
QY 121 LPGRNTSPDNTYLYWHRSLKIHQCNIFREGQYFGCSFDLTWKVDSFQHSVQIMV 180
DB 147 LPGRNTSPDNTYLYWHRSLKIHQCNIFREGQYFGCSFDLTWKVDSFQHSVQIMV 206
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYQWENPQNFISRCLEFYEVEVNN 240
DB 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYQWENPQNFISRCLEFYEVEVNN 266
QY 241 SQTETHNVFYVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNLCYEDDKL 300
DB 267 SQTETHNVFYVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNLCYEDDKL 326
QY 301 WSNWSQEMSGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLKLKXIIIPPPDPGKIFK 360
DB 327 WSNWSQEMSGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLKLKXIIIPPPDPGKIFK 386
QY 361 EMFGDQNDTLHWKXYDIYEKQTEETDSVVLJENLKASQ 401
DB 387 EMFGDQNDTLHWKXYDIYEKQTEETDSVVLJENLKASQ 427

RESULT 5
ADL71812
XX ADL71812 standard; protein; 427 AA.
AC ADL71812;
DT 20-MAY-2004 (first entry)
XX Human interleukin-13 receptor alpha (IL-13 Ralpha) protein.
DE Human; IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis;
KW eczema; asthma; AIDS; gene therapy; interleukin; receptor.
XX Homo sapiens.
OS
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Qy	301	WSNWSQMSIGKKNSTLYITMLLIVPVIVAGAIIVLLVLRKLIIFPPIDPGKIFK	360
Db	327	WSNWSQMSIGKKNSTLYITMLLIVPVIVAGAIIVLLVLRKLIIFPPIDPGKIFK	386
Qy	361	EMFGDQNDTLHWKKYDIYEKQTKETDSVVLLENLAKASQ	401
Db	387	EMFGDQNDTLHWKKYDIYEKQTKETDSVVLLENLAKASQ	427
RESULT 6			
ADL82843	ADL82843 standard; protein; 427 AA.		
XX	AC	ADL82843;	
XX	DT	17-JUN-2004 (first entry)	
XX	DE	Human PRO2537, SEQ ID 45.	
XX	XX	Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;	
KW	KW	Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;	
KW	KW	Gene Therapy; PRO; B cell related disorder; cancer;	
KW	KW	immune-mediated inflammatory disease; human.	
XX	OS	Homo sapiens.	
XX	XX	WO2004024097-A2.	
XX	XX	25-MAR-2004.	
XX	XX	15-SEP-2003; 2003WO-US029097.	
XX	XX	16-SEP-2002; 2002US-0411392P.	
XX	PA	(GETH) GENENTECH INC.	
XX	XX	Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;	
PI	PI	Wu TD;	
XX	XX	WPI; 2004-329389/30.	
DR	DR	N-PSDB; ADL82842.	
XX	XX	New PRO polypeptide, useful for diagnosing and treating a B cell related	
PT	PT	disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune	
PT	PT	mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.	
XX	XX	Claim 10; Fig 45; 695pp; English.	
XX	XX	The present invention relates to PRO proteins and their coding sequences.	
CC	CC	The PRO proteins are useful for diagnosing and treating a B cell related	
CC	CC	disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide	
CC	CC	antigen unresponsiveness, selective IgA deficiency, selective IgM	
CC	CC	deficiency, selective deficiency of IgG subclasses, immunodeficiency with	
CC	CC	hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's	
CC	CC	lymphoma, intermediate lymphoma, follicular lymphoma, type II	
CC	CC	hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic	
CC	CC	anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or	
CC	CC	ankylosing spondylitis. The PRO proteins are also useful for preparing a	
CC	CC	medicament for treating a condition that is responsive to the PRO	
CC	CC	protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO	
CC	CC	coding sequences are useful as hybridization probes in chromosome and	
CC	CC	gene mapping, in preparing PRO proteins, or in generating transgenic	
CC	CC	animals or knockout animals, which in turn are useful in the development	
CC	CC	and screening of therapeutically useful reagents.	
XX	XX	Sequence 427 AA;	
Query Match			
Best Local Similarity 100.0%; Score 2172; DB 8; Length 427;			
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSHFGDKQDKKIAPETRRSI	60

Db	27	APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSHFGDKQDKKIAPETRRSI	86
Qy	61	EVPLNERICLOVGSQSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW	120
Db	87	EVPLNERICLOVGSQSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW	146
Qy	121	LPGRNTSPDNTYLYWHRSLKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV	180
Db	147	LPGRNTSPDNTYLYWHRSLKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV	206
Qy	181	KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLYVQWENPQNFISCLFYEVEVNN	240
Db	207	KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLYVQWENPQNFISCLFYEVEVNN	266
Qy	241	SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDLTNTVIRVTKNKLCEYEDDKL	300
Db	267	SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDLTNTVIRVTKNKLCEYEDDKL	326
Qy	301	WSNWSQMSIGKKNSTLYITMLLIVPVIVAGAIIVLLVLRKLIIFPPIDPGKIFK	360
Db	327	WSNWSQMSIGKKNSTLYITMLLIVPVIVAGAIIVLLVLRKLIIFPPIDPGKIFK	386
Qy	361	EMFGDQNDTLHWKKYDIYEKQTKETDSVVLLENLAKASQ	401
Db	387	EMFGDQNDTLHWKKYDIYEKQTKETDSVVLLENLAKASQ	427
RESULT 7			
ADN04504	ADN04504 standard; protein; 427 AA.		
XX	AC	ADN04504;	
XX	DT	01-JUL-2004 (first entry)	
XX	DE	Antipsoriatic protein sequence #445.	
XX	XX	antipsoriatic; gene therapy; psoriasis; diagnosis.	
XX	OS	Homo sapiens.	
XX	XX	WO2004028479-A2.	
XX	XX	08-APR-2004.	
XX	XX	25-SEP-2003; 2003WO-US030907.	
XX	XX	25-SEP-2002; 2002US-0414006P.	
XX	XX	(GETH) GENENTECH INC.	
XX	XX	Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;	
PI	PI	Wu TD;	
XX	XX	WPI; 2004-305105/28.	
DR	DR	N-PSDB; ADN04503.	
XX	XX	New PRO nucleic acid or polypeptide, useful for preparing a	
PT	PT	pharmaceutical composition for diagnosing or treating psoriasis in a	
PT	PT	mammal.	
XX	XX	Claim 9; SEQ ID NO 898; 3069pp; English.	
PS	PS	The invention relates to novel polynucleotide and polypeptides for	
CC	CC	treating psoriasis or a sequence having at least 80% identity to the	
CC	CC	above sequences. The nucleic acid is useful for preparing a composition	
CC	CC	for diagnosing or treating psoriasis in a mammal. This sequence	
CC	CC	corresponds to one of the polypeptides of the invention.	
XX	XX	Sequence 427 AA;	
Query Match			
Best Local Similarity 100.0%; Score 2172; DB 8; Length 427;			
Matches 401; Conservative 100.0%; Pred. No. 3.3e-201;			

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 APTETQPPVTNLVSVENLCTVIWTWNPPEGASNCSLWTFSHFGDKQDKKIAPETRRSI 60
Db	
QY	27 APTETQPPVTNLVSVENLCTVIWTWNPPEGASNCSLWTFSHFGDKQDKKIAPETRRSI 86
Db	
QY	61 EVPLNERICLVGSGQCSSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120
Db	
QY	87 EVPLNERICLVGSGQCSSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 146
Db	
QY	121 LPGRNTSPDNTYLYWHSLEKIHQCENIFREGQYFGCSFDLTWKVDSSFEQHSQIMV 180
Db	
QY	147 LPGRNTSPDNTYLYWHSLEKIHQCENIFREGQYFGCSFDLTWKVDSSFEQHSQIMV 206
Db	
QY	181 KDNAGKIKPSFNIVPLTSRVKDPDPHINKLSFNHDDLQVQWENPQNFISRCLFYFEVEVNN 240
Db	
QY	207 KDNAGKIKPSFNIVPLTSRVKDPDPHINKLSFNHDDLQVQWENPQNFISRCLFYFEVEVNN 266
Db	
QY	241 SQTETHNVFYQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVRIRVTKNKLCYEDDKL 300
Db	
QY	267 SQTETHNVFYQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVRIRVTKNKLCYEDDKL 326
Db	
QY	301 WSNWSQEMSIGKKRNSTLYITMLLIVPVI VAGAIIVLLLYLKLKIIIPPIPDGKIFK 360
Db	
QY	327 WSNWSQEMSIGKKRNSTLYITMLLIVPVI VAGAIIVLLLYLKLKIIIPPIPDGKIFK 386
Db	
QY	361 EMFGDQNDTLHWKKYDIYEKQTKETSDSVLIENLKASQ 401
Db	
QY	387 EMFGDQNDTLHWKKYDIYEKQTKETSDSVLIENLKASQ 427
Db	
RESULT 8	
ADN62575	
ID	ADN62575 standard; protein; 427 AA.
XX	
AC	ADN62575;
XX	
DT	12-AUG-2004 (first entry)
XX	
DE	Human interleukin 13 (IL-13) receptor alpha 1 chain.
XX	
KW	Human; receptor; cytokine; interleukin 13 receptor alpha 1 chain; IL-13;
KW	IL-4; atopy; atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;
KW	cancer; inflammatory disease; rheumatoid arthritis;
KW	Lupus erythematosus; multiple sclerosis; Alzheimer's disease;
KW	urticaria; nephrotic syndrome; glomerulonephritis; ulcerative colitis;
KW	Crohn's disease; Sjogren's syndrome; toxoplasmosis; listeriosis; leprosy;
KW	Lyme disease; tuberculosis; malaria; leishmaniasis.
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Peptide 1..26
FT	/notes="Signal peptide"
FT	27..427
FT	/note="Mature protein claimed in claim 1"
XX	
PN	US6743604-B1.
XX	
PD	01-JUN-2004.
XX	
XX	06-APR-2000; 2000US-00545002.
XX	
PR	13-DEC-1996; 96GB-00025899.
PR	12-NOV-1997; 97US-00969125.
XX	
FA	(SMIK) SMITHKLINE BEECHAM CORP.
XX	
PI	Bonnefoy J, Gauchat J;
XX	
DR	WPI; 2004-409324/38.
XX	
DR	N-PSDB; ADN62574.
XX	

XX	New isolated nucleic acid molecule encoding a polypeptide capable of binding human IL-13 and/or binding human IL-4, useful in medicine, in diagnostics or for producing antibodies.
PT	
PT	
XX	
PS	Claim 1; SEQ ID NO 9; 24pp; English.
XX	
CC	The invention relates to an isolated nucleic acid molecule (ADN62574), which encodes the mature form of a polypeptide capable of binding human IL-13 (interleukin 13, a cytokine) and/or binding human IL-4 (designated IL-13 receptor alpha 1 subunit) appearing as ADN62575. Also included are a vector comprising the nucleic acid molecule and a host cell comprising the vector. The nucleic acids are useful as probes or primers or in the analysis of allelic variation. The polypeptides are useful for binding human IL-13 and/or binding human IL-4 and act as inhibitors by interfering with the interaction between human IL-13 or IL-4 and their natural receptors. They can also be used in medicine, e.g. for treatment of diseases such as atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma, AIDS, cancer, inflammatory disease (e.g. rheumatoid arthritis and inflammatory bowel disease), multiple sclerosis, uveitis, psoriasis, lupus erythematosus, thyroiditis, diabetes, arthritis, ulcerative colitis, urticaria, nephrotic syndrome, glomerulonephritis, listeriosis, leprosy, Crohn's disease, Sjogren's syndrome, toxoplasmosis, malaria, eczema, Lyme disease, tuberculosis, malaria and leishmaniasis. They can also be used for producing antibodies, which can be used for diagnosing diseases. The present sequence represents IL-13 receptor alpha 1 subunit.
CC	
XX	
SQ	Sequence 427 AA;
Query Match 100.0%; Score 2172; DB 8; Length 427;	
Best Local Similarity 100.0%; Pred. No. 3.3e-201;	
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 APTETQPPVTNLVSVENLCTVIWTWNPPEGASNCSLWTFSHFGDKQDKKIAPETRRSI 60
Db	
QY	27 APTETQPPVTNLVSVENLCTVIWTWNPPEGASNCSLWTFSHFGDKQDKKIAPETRRSI 86
Db	
QY	61 EVPLNERICLVGSGQCSSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120
Db	
QY	87 EVPLNERICLVGSGQCSSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 146
Db	
QY	121 LPGRNTSPDNTYLYWHSLEKIHQCENIFREGQYFGCSFDLTWKVDSSFEQHSQIMV 180
Db	
QY	147 LPGRNTSPDNTYLYWHSLEKIHQCENIFREGQYFGCSFDLTWKVDSSFEQHSQIMV 206
Db	
QY	181 KDNAGKIKPSFNIVPLTSRVKDPDPHINKLSFNHDDLQVQWENPQNFISRCLFYFEVEVNN 240
Db	
QY	207 KDNAGKIKPSFNIVPLTSRVKDPDPHINKLSFNHDDLQVQWENPQNFISRCLFYFEVEVNN 266
Db	
QY	241 SQTETHNVFYQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVRIRVTKNKLCYEDDKL 300
Db	
QY	267 SQTETHNVFYQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVRIRVTKNKLCYEDDKL 326
Db	
QY	301 WSNWSQEMSIGKKRNSTLYITMLLIVPVI VAGAIIVLLLYLKLKIIIPPIPDGKIFK 360
Db	
QY	327 WSNWSQEMSIGKKRNSTLYITMLLIVPVI VAGAIIVLLLYLKLKIIIPPIPDGKIFK 386
Db	
QY	361 EMFGDQNDTLHWKKYDIYEKQTKETSDSVLIENLKASQ 401
Db	
QY	387 EMFGDQNDTLHWKKYDIYEKQTKETSDSVLIENLKASQ 427
Db	
RESULT 9	
ABM82441	
ID	ABM82441 standard; protein; 427 AA.
XX	
AC	ABM82441;
XX	
DT	18-NOV-2004 (first entry)
XX	
DE	Tumour-associated antigenic target (TAT) polypeptide PRO2537, SEQ:6271.
XX	
KW	Tumour-associated antigenic target; TAT; human; overexpression; cancer;

tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytostatic.

Homo sapiens.

WO2004030615-A2.

15-APR-2004.

29-SEP-2003; 2003WO-US028547.

02-OCT-2002; 2002US-0414971P.

(GETH) GENENTECH INC.

Wu TD, Zhang Z, Zhou Y;

WPI; 2004-347921/32.

N-PSDB; ACN41073.

New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or prostate cancer or tumor.

Claim 12; SEQ ID NO 6271; 7273pp; English.

The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT polypeptide of the invention

Sequence 427 AA;

Query Match 100.0%; Score 2172; DB 8; Length 427;

Best Local Similarity 100.0%; Pred. NO. 3.3e-201;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APETQPPVTLNLSVSNELCTVIWTPNPEGASSCSLWYFSGHFGDKQDKKIAPETRSL 60

DB 27 APETQPPVTLNLSVSNELCTVIWTPNPEGASSCSLWYFSGHFGDKQDKKIAPETRSL 86

QY 61 EYPLNERICLVQGSQCSTNESKPSILVEKCISSPEGDPESAVTELQCIWHNLSYMKCSW 120

DB 87 EYPLNERICLVQGSQCSTNESKPSILVEKCISSPEGDPESAVTELQCIWHNLSYMKCSW 146

QY 121 LFGRTSPDNTYLYWHRSLKIHQCEINIFREGQYFGCSFDLTQVQDSSFEQHSVQIMV 180

DB 147 LFGRTSPDNTYLYWHRSLKIHQCEINIFREGQYFGCSFDLTQVQDSSFEQHSVQIMV 206

QY 181 KDNAGKIKPSNIVPLTSRVKDPDPHINKLSFNHNDLYVQWENPNQFISRCILFYEVVNN 240

DB 207 KDNAGKIKPSNIVPLTSRVKDPDPHINKLSFNHNDLYVQWENPNQFISRCILFYEVVNN 266

QY 241 SQTEHNVFYVQBAKCNPFERNVENTSCFMVPGVLPDLTNTVIRVKNKLCYEDDKL 300

DB 267 SQTEHNVFYVQBAKCNPFERNVENTSCFMVPGVLPDLTNTVIRVKNKLCYEDDKL 326

QY 301 WSNWSQMSIGKGRNSTLYITMLLIIVPVIVAGAIIVLLLYLKRUKLIIFPPIDPGKIFK 360

DB 327 WSNWSQMSIGKGRNSTLYITMLLIIVPVIVAGAIIVLLLYLKRUKLIIFPPIDPGKIFK 386

QY 361 EMFGDQNDTTLHWKKYDIYKQTKETDSVVLIENLKKASQ 401

DB 387 EMFGDQNDTTLHWKKYDIYKQTKETDSVVLIENLKKASQ 427

RESULT 10

ADL71813

ID ADL71813 standard; protein; 427 AA.

XX AC ADL71813;

XX DT 20-MAY-2004 (first entry)

XX DE Human interleukin-13 receptor alpha (IL-13 Ralpha) mutant, T1301.

XX KW Human; IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS; gene therapy; interleukin; receptor; mutant;

XX KW mutein.

XX OS Homo sapiens.

OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 130 /note= "Wild-type Thr is substituted with Ile"

XX PN US2004043921-A1.

XX PD 04-MAR-2004.

XX PF 29-SEP-2003; 2003US-00671697.

XX PR 13-DEC-1996; 96GB-00025899.

PR 12-NOV-1997; 97US-00969125.

XX PR 06-APR-2000; 2000US-00545002.

XX PA (BONN/) BONNEFOY J.

XX PI (GAUC/) GAUCHAT J.

XX PI Bonnefoy J, Gauchat J;

XX DR WPI; 2004-225726/21.

XX PT Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma or AIDS, comprises administering a polypeptide or soluble polypeptide.

XX PS Claim 14; Page; 27pp; English.

XX CC The invention relates to polypeptides capable of binding human interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpha. The invention also relates to a method of treatment of a disease in which IL13 and IL4 cause adverse effects. The method is useful for treating a disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides of the invention are useful in raising antibodies. It is also useful in gene therapy. The present sequence is human interleukin-13 receptor alpha (IL-13 Ralpha) mutant protein. Note: This sequence is not shown in the CC specification, however it is constructed based on human IL-13 Ralpha protein shown as SEQ ID NO:9 in the specification.

XX SQ Sequence 427 AA;

Query Match 99.7%; Score 2166; DB 8; Length 427;

Best Local Similarity 99.8%; Pred. No. 1.3e-200;				
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
Qy	1	APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFGDKQDKKIAPETRRI	60	
Db	27	APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFGDKQDKKIAPETRRI	86	
Qy	61	EVPLNERICLVQSGQCSSTNESEKPSILVEKCIIPPEGDPESAVTELOCIWHNLSYMKCSW	120	
Db	87	EVPLNERICLVQSGQCSSTNESEKPSILVEKCIIPPEGDPESAVTELOCIWHNLSYMKCSW	146	
Qy	121	LPGRNTSPDTNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFEGHSQIWMV	180	
Db	147	LPGRNTSPDTNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFEGHSQIWMV	206	
Qy	181	KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCIFYEVEVNN	240	
Db	207	KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCIFYEVEVNN	266	
Qy	241	SQTETHNVFVQKACENPEFERNVENTSCFMVPGVLPDTLNTVTRIRVTKNLCYEDDKL	300	
Db	267	SQTETHNVFVQKACENPEFERNVENTSCFMVPGVLPDTLNTVTRIRVTKNLCYEDDKL	326	
Qy	301	WSNWSQEMSIGKRNSTLYITMLLIVPVIVAGAIIVLLVLLKRLKIIIFPPIDPGKIFK	360	
Db	327	WSNWSQEMSIGKRNSTLYITMLLIVPVIVAGAIIVLLVLLKRLKIIIFPPIDPGKIFK	386	
Qy	361	EMFGDQNDTLLHWKKYDIYEKQTKETDSVVLJENLKASQ	401	
Db	387	EMFGDQNDTLLHWKKYDIYEKQTKETDSVVLJENLKASQ	427	
RESULT 11				
ID	ADF17835	;		
AC	ADF17835	standard; protein; 427 AA.		
XX	ADF17835;			
DT	12-FEB-2004	(first entry)		
DE	Human IL-13 alpha 1 receptor (IL-13R) protein.			
KW	IL-13R; human; receptor; anaphylaxis; hay fever; asthma;			
KW	antiflammatory; cytostatic; antiulcer; dermatological; antiallergic;			
KW	antisthmatic; fibrosis; Hodgkin's disease; ulcerative colitis;			
KW	scleroderma; allergic rhinitis; oncological;			
KW	chronic obstructive pulmonary disease.			
OS	Homo sapiens.			
XX	WO2003080675-A2.			
PN				
XX	02-OCT-2003.			
PF				
XX	21-MAR-2003; 2003WO-AU000352.			
XX				
PR	22-MAR-2002; 2002AU-00001301.			
PR	03-FEB-2003; 2003AU-00900437.			
XX				
XX	(AMRA-) AMRAD OPERATIONS PTY LTD.			
PA				
XX	Dunlop FM, Baca M, Nash AD, Fabri LJ;			
PI				
XX	WPI; 2003-876912/81.			
DR	N-PSDB; ADF17834.			
DR				
XX	New monoclonal antibodies against interleukin-13 receptor alpha, useful			
PT	for treating fibrosis, Hodgkin's disease, ulcerative colitis,			
PT	scleroderma, allergic rhinitis, oncological conditions, asthma or an			
PT	inflammatory disorder.			
XX				
XX	Disclosure; SEQ ID NO 4; 99pp; English.			
PS				
XX				
This invention relates to a novel antibodies that function as interleukin				
-13 receptor alpha-1 chain (IL-13R alpha-1) antagonists and can be used				
for treating certain conditions induced by IL-13. Specifically, it refers				
to antibodies that bind to IL-13R alpha-1 and inhibit or modulate IL-13				
and IL-4 induced signalling. IL-13 is a mediator in the immunostimulatory				
system, such that it is involved in the induction of IGE, IgG4 and T-				
helper cells and accordingly is implicated in conditions from anaphylaxis				
to hay fever and asthma. As such, the present invention describes these				
novel antibodies as antiinflammatory, cytostatic, antiulcer,				
dermatological, antiallergic and antiasthmatic. The methods and				
compositions are useful for treating various disorders including				
fibrosis, Hodgkin's disease, ulcerative colitis, scleroderma, allergic				
rhinitis, oncological conditions and chronic obstructive pulmonary				
disease. This polypeptide sequence is the human IL-13 alpha 1 receptor				
protein of the invention.				
XX				
SQ	Sequence 427 AA;			
Query Match 99.7%; Score 2165; DB 7; Length 427;				
Best Local Similarity 99.8%; Pred. No. 1.6e-200;				
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
Qy	1	APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFGDKQDKKIAPETRRI	60	
Db	27	APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFGDKQDKKIAPETRRI	86	
Qy	61	EVPLNERICLVQSGQCSSTNESEKPSILVEKCIIPPEGDPESAVTELOCIWHNLSYMKCSW	120	
Db	87	EVPLNERICLVQSGQCSSTNESEKPSILVEKCIIPPEGDPESAVTELOCIWHNLSYMKCSW	146	
Qy	121	LPGRNTSPDTNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFEGHSQIWMV	180	
Db	147	LPGRNTSPDTNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFEGHSQIWMV	206	
Qy	181	KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCIFYEVEVNN	240	
Db	207	KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCIFYEVEVNN	266	
Qy	241	SQTETHNVFVQKACENPEFERNVENTSCFMVPGVLPDTLNTVTRIRVTKNLCYEDDKL	300	
Db	267	SQTETHNVFVQKACENPEFERNVENTSCFMVPGVLPDTLNTVTRIRVTKNLCYEDDKL	326	
Qy	301	WSNWSQEMSIGKRNSTLYITMLLIVPVIVAGAIIVLLVLLKRLKIIIFPPIDPGKIFK	360	
Db	327	WSNWSQEMSIGKRNSTLYITMLLIVPVIVAGAIIVLLVLLKRLKIIIFPPIDPGKIFK	386	
Qy	361	EMFGDQNDTLLHWKKYDIYEKQTKETDSVVLJENLKASQ	401	
Db	387	EMFGDQNDTLLHWKKYDIYEKQTKETDSVVLJENLKASQ	427	
RESULT 12				
ID	ADL71814	standard; protein; 427 AA.		
XX	ADL71814;			
AC	ADL71814;			
XX				
DT	20-MAY-2004	(first entry)		
XX				
DE	Human interleukin-13 receptor alpha (IL-13 Ralpha) mutant, G358D.			
XX				
XX	Human; IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis;			
KW	eczema; asthma; AIDS; gene therapy; interleukin; receptor; mutant;			
KW	muten.			
XX	Homo sapiens.			
OS	Synthetic.			
XX				
XX	Key	Location/Qualifiers		
PH	Misc-difference 358			
FT	/note= "Wild-type Gly is substituted with Asp"			
XX				
PN	US2004043921-A1.			

```
XX 04-MAR-2004.
XX 29-SEP-2003; 2003US-00671697.
XX 13-DEC-1996; 96GB-00025899.
XX 12-NOV-1997; 97US-00969125.
XX 06-APR-2000; 2000US-00545002.
XX (BONN/) BONNEFOY J.
XX (GAUC/) GAUCHAT J.
XX Bonnefoy J, Gauchat J;
XX WPI; 2004-225726/21.
XX
XX Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse
XX effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma
XX or AIDS, comprises administering a polypeptide or soluble polypeptide.
XX
XX Claim 14; Page; 27pp; English.
XX
XX The invention relates to polypeptides capable of binding human
XX interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpha. The
XX invention also relates to a method of treatment of a disease in which
XX IL13 and IL4 cause adverse effects. The method is useful for treating a
XX disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic
XX dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides
XX of the invention are useful in raising antibodies. It is also useful in
XX gene therapy. The present sequence is human interleukin-13 receptor alpha
XX (IL-13 Ralpha) mutant protein. Note: This sequence is not shown in the
XX specification, however it is constructed based on human IL-13 Ralpha
XX protein shown as SEQ ID NO:9 in the specification.
XX
XX Sequence 427 AA;
XX
XX Query Match 99.7%; Score 2165; DB 8; Length 427;
XX Best Local Similarity 99.8%; Pred. No. 1.6e-200; Indels 0; Gaps 0;
XX Matches 400; Conservative 0; Mismatches 1;
XX
XX 1 APTQTQPTVNLVSVENLCTVIWTWNPPEGASSNCSLWYFHFSGDKQDKKIAPEPTRSI 60
XX 27 APTQTQPTVNLVSVENLCTVIWTWNPPEGASSNCSLWYFHFSGDKQDKKIAPEPTRSI 86
XX
XX 61 EVPLNERICLVGSCQSNSEKPSILVEKICISPPGDPESAVTELCIWNLSYMKCSW 120
XX 87 EVPLNERICLVGSCQSNSEKPSILVEKICISPPGDPESAVTELCIWNLSYMKCSW 146
XX
XX 121 LPRGNTSPDNTYLLYHRSLEKIHOCENIPREGYFGCSFDLTQVKDSSFEQHSVQIMV 180
XX 147 LPRGNTSPDNTYLLYHRSLEKIHOCENIPREGYFGCSFDLTQVKDSSFEQHSVQIMV 206
XX
XX 181 KDNAGKIPSFNIVPLTSRVKPDPPHINKNLSFHNDDLVQVENPQNFISRCILFYEVEVNN 240
XX 207 KDNAGKIPSFNIVPLTSRVKPDPPHINKNLSFHNDDLVQVENPQNFISRCILFYEVEVNN 266
XX
XX 241 SQTETHNVFYVQKACNPEPERNVENTSCFMVPGVLPDNLNTRVIRVKTNKLCEYDDKL 300
XX 267 SQTETHNVFYVQKACNPEPERNVENTSCFMVPGVLPDNLNTRVIRVKTNKLCEYDDKL 326
XX
XX 301 WSNWQEMSIGKRNSTLYITMLLIVPVIVAGAIIVLLYLKRLKIIIPFPDPGKIFK 360
XX 327 WSNWQEMSIGKRNSTLYITMLLIVPVIVADAIIVLLYLKRLKIIIPFPDPGKIFK 386
XX
XX 361 EMFGQNDTLLHWKYDYIEKQTKETDSVLIENLKKASQ 401
XX 387 EMFGQNDTLLHWKYDYIEKQTKETDSVLIENLKKASQ 427
XX
XX RESULT 13
XX AAB19808
XX ID AAB19808 standard; protein; 427 AA.
XX
```

```
AC AAB19808;
XX 05-MAR-2001 (first entry)
XX Human interleukin-13 receptor alpha-1 variant.
XX
XX Interleukin-13 receptor alpha-1; interleukin-4; human; atopy;
XX atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;
XX dermatological; antiasthmatic; antiallergic; therapy; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..26
XX /label= Sig_peptide
XX Domain 27..347
XX /label= Extracellular_domain
XX Protein 28..427
XX /label= Mature_protein
XX Misc-difference 130
XX /note= "Gly in "
XX Peptide 327..331
XX /note= "NSXWS motif conserved in the type-I cytokine
XX receptor superfamily"
XX Domain 348..367
XX /label= Transmembrane_domain
XX Domain 368..427
XX /label= Cytoplasmic_domain
XX Binding-site 405..408
XX /note= "YXXQ motif, consensus for STAT binding"
XX
XX US6143871-A.
XX
XX 07-NOV-2000.
XX
XX 12-NOV-1997; 97US-00969125.
XX
XX 13-DEC-1996; 96GB-00025899.
XX (GAUC/) GAUCHAT J.
XX (BONN/) BONNEFOY J.
XX
XX Gauchat J, Bonnefoy J;
XX
XX WPI; 2001-006445/01.
XX
XX Novel polypeptide capable of binding interleukin-13 or interleukin-4
XX useful for treating atopy, atopic dermatitis, allergies, rhinitis,
XX eczema, asthma or AIDS.
XX
XX Claim 4; -; 26pp; English.
XX
XX The present sequence is that of a claimed isolated polypeptide which is
XX capable of binding human interleukin-13 (IL-13) and/or human interleukin-
XX 4 (IL-4) in the presence of IL-4 receptor alpha. It differs from a
XX sequence (see AAB19807) deduced from isolated cDNA by having residue 130
XX as Ile rather than Thr and residue 358 as Asp rather than Gly. This IL-13
XX receptor alpha-1 polypeptides can be used to inhibit IL-13 or IL-4
XX induced IgE synthesis in B cells, useful in the treatment of diseases in
XX which IgE or Th2 differentiation plays a role, e.g. atopy, atopic
XX dermatitis, allergy, rhinitis, eczema, asthma or AIDS. Antibodies raised
XX against the polypeptide are useful for detecting IL-13 and IL-4 receptor
XX or parts of them which have been shed from cells as a result of disease,
XX e.g. cancer, leukaemia, atopy, atopic dermatitis, allergies, rhinitis,
XX eczema, asthma, lupus erythematosus, AIDS, thyroiditis, diabetes,
XX uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome,
XX inflammatory bowel disease, glomerulonephritis, ulcerative colitis,
XX Crohn's disease, Sjogren's syndrome and toxoplasmosis. Note: The present
XX sequence is not shown in the specification but is derived from the IL-13
XX receptor alpha 1 sequence given in figure 1 (see AAB19807)
XX
XX Sequence 427 AA;
```

```
Query Match      99.4%; Score 2159; DB 4; Length 427;
Best Local Similarity 99.5%; Pred. No. 6.1e-200;
Matches 399; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 APTETQPPVNLVSVENLCTVIWTWNPPEGASNSCLWTFSHFGDKQDKKIAPETRISI 60
DB 27 APTETQPPVNLVSVENLCTVIWTWNPPEGASNSCLWTFSHFGDKQDKKIAPETRISI 86
QY 61 EVPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 120
DB 87 EVPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 146
QY 121 LPGNTSPDNTYLTYYWHSLSLEKIHQENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 180
DB 147 LPGNTSPDNTYLTYYWHSLSLEKIHQENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 206
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLIVQWENPQNFISCLFYEVEVNN 240
DB 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLIVQWENPQNFISCLFYEVEVNN 266
QY 241 SQTETHNVFVQEAACENPFRNVENTSCFMVPGVLPDLTNTVIRVKTNKLCEYEDDKL 300
DB 267 SQTETHNVFVQEAACENPFRNVENTSCFMVPGVLPDLTNTVIRVKTNKLCEYEDDKL 326
QY 301 WSNWSQEMSIGKKNSTLYITMLLIVPVI VAGAIIVLLLYLKLKIIIFPPIDPGKIFK 360
DB 327 WSNWSQEMSIGKKNSTLYITMLLIVPVI VADAIIVLLLYLKLKIIIFPPIDPGKIFK 386
QY 361 EMFGQNDTTLHWKDYDIYEKQTEEDTSVVLLENLKKASQ 401
DB 387 EMFGQNDTTLHWKDYDIYEKQTEEDTSVVLLENLKKASQ 427

RESULT 14
AAU69132
ID AAU69132 standard; protein; 405 AA.
AC AAU69132;
XX
XX 29-JAN-2002 (first entry)
XX
XX Canine interleukin 13 receptor PcaIL-13Ra1pha1 405.
XX
XX Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
XX IL-13Ra1pha1; IR-13Ra1pha2; immunoglobulin heavy chain; IGG Fc;
XX immunoglobulin light chain; lambda; immunosuppressive; gene therapy;
XX immune response.
XX
XX Canis familiaris.
XX
XX WO200177332-A2.
XX
XX 18-OCT-2001.
XX
XX 09-APR-2001; 2001WO-US011498.
XX
XX 07-APR-2000; 2000US-0195659P.
XX 07-APR-2000; 2000US-0195874P.
XX
XX (HESK-) HESKA CORP.
XX
XX McCall CA, Tang L;
XX
XX WPI; 2001-657172/75.
XX
XX N-PSDB; AAS59954, AAS59956.
XX
XX Novel isolated canine protein, preferably canine immunoglobulin G protein
XX or canine interleukin-13 receptor protein useful for regulating immune
XX response of an animal and for developing regulatory compounds.
XX
XX Claim 18; Page 164-165; 221pp; English.
XX
XX The invention concerns an isolated canine protein, preferably canine
```

```
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13) receptor
CC protein, the nucleic acids encoding them, antibodies raised against them,
CC fusion proteins between the IGG and IL-13R proteins and methods of
CC isolating regulators of them. The regulators are useful for regulating an
CC immune response in a canine. The proteins useful to develop regulatory
CC compounds including inhibitors and activators that, when administered to
CC a canine in an effective manner, are capable of protecting canine from
CC disease mediated by IL-13Ra1pha or IL-13. The regulators are useful for
CC treating canine IGG (heavy and/or light chain) and/or canine IL-13R
CC mediated responses. The molecules of the invention are useful to regulate
CC the immune response of an animal (e.g. by gene therapy). The present
CC sequence represents a protein of the invention
XX
XX Sequence 405 AA;
SQ

Query Match      86.0%; Score 1869; DB 4; Length 405;
Best Local Similarity 85.5%; Pred. No. 7.1e-172;
Matches 343; Conservative 24; Mismatches 34; Indels 0; Gaps 0;

QY 1 APTETQPPVNLVSVENLCTVIWTWNPPEGASNSCLWTFSHFGDKQDKKIAPETRISI 60
DB 5 APTETQPPVNLVSVENLCTVIWTWNPPEGASNSCLWTFSHFGDKQDKKIAPETRISK 64
QY 61 EVPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 120
DB 65 EVPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCTW 124
QY 121 LPGNTSPDNTYLTYYWHSLSLEKIHQENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 180
DB 125 LPGNTSPDNTYLTYYWHSLSLEKIHQENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 184
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLIVQWENPQNFISCLFYEVEVNN 240
DB 185 KDNARKIRPSFNIVPLTSRVKPPPHIKRLLFFQGNLYVQMKNPQNFYSRCLSYQVEVNN 244
QY 241 SQTETHNVFVQEAACENPFRNVENTSCFMVPGVLPDLTNTVIRVKTNKLCEYEDDKL 300
DB 245 SQTETHNVFVQEAACENPFRNVENTSCFMVPGVLPDLTNTVIRVKTNKLCEYEDDKL 304
QY 301 WSNWSQEMSIGKKNSTLYITMLLIVPVI VAGAIIVLLLYLKLKIIIFPPIDPGKIFK 360
DB 305 WSNWSQAMSGENTDPTFYITMLLATQVIVAGAIIVLLLYLKLKIIIFPPIDPGKIFK 364
QY 361 EMFGQNDTTLHWKDYDIYEKQTEEDTSVVLLENLKKASQ 401
DB 365 EMFGQNDTTLHWKDYDIYEKQTEEDTSVVLLENLKKASQ 405

RESULT 15
ADF17841
ID ADF17841 standard; protein; 664 AA.
XX
XX ADF17841;
XX
XX 12-FEB-2004 (first entry)
XX
XX Chimeric human IL-13R alpha 1-gp130 fusion protein.
XX
XX IL-13R alpha 1-gp130; human; receptor; chimeric; anaphylaxis; hay fever;
XX asthma; antiinflammatory; cytostatic; antiulcer; dermatological;
XX antiallergic; antiasthmatic; fibrosis; Hodgkin's disease;
XX ulcerative colitis; scleroderma; allergic rhinitis; oncological;
XX chronic obstructive pulmonary disease.
XX
XX Chimeric.
XX
XX Homo sapiens.
XX
XX WO2003080675-A2.
XX
XX 02-OCT-2003.
XX
XX 21-MAR-2003; 2003WO-AU000352.
XX
```


PR 22-MAR-2002; 2002AU-00001301.
PR 03-FEB-2003; 2003AU-00900437.
XX
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Dunlop FM, Baca M, Nash AD, Fabri LJ;
XX
XX WPI; 2003-876912/81.
XX N-PSDB; ADF17840.
XX
XX New monoclonal antibodies against interleukin-13 receptor alpha, useful
XX for treating fibrosis, Hodgkin's disease, ulcerative colitis,
XX scleroderma, allergic rhinitis, oncological conditions, asthma or an
XX inflammatory disorder.
XX
XX Disclosure; SEQ ID NO 10; 99pp; English.
XX
XX This invention relates to a novel antibodies that function as interleukin
XX -13 receptor alpha-1 chain (IL-13R alpha-1) antagonists and can be used
XX for treating certain conditions induced by IL-13. Specifically, it refers
XX to antibodies that bind to IL-13R alpha-1 and inhibit or modulate IL-13
XX and IL-4 induced signalling. IL-13 is a mediator in the immunostimulatory
XX system, such that it is involved in the induction of IgE, IgG4 and T-
XX helper cells and accordingly is implicated in conditions from anaphylaxis
XX to hay fever and asthma. As such, the present invention describes these
XX novel antibodies as antiinflammatory, cytostatic, antiulcer,
XX dermatological, antiallergic and antiasthmatic. The methods and
XX compositions are useful for treating various disorders including
XX fibrosis, Hodgkin's disease, ulcerative colitis, scleroderma, allergic
XX rhinitis, oncological conditions and chronic obstructive pulmonary
XX disease. This polypeptide sequence is the chimeric human IL-13R alpha 1-
XX gp130 fusion protein of the invention.
XX
XX Sequence 664 AA;
XX
XX Query Match : 82.2%; Score 1784.5; DB 7; Length 664;
XX Best Local Similarity 91.7%; Pred. No. 2.3e-163;
XX Matches 333; Conservative 8; Mismatches 15; Indels 7; Gaps 3;
XX
XX 1 APTETQPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFSHFQDKQDKKIAPETRRSI 60
XX 45 APTETQPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFSHFQDKQDKKIAPETRRSI 104
XX
XX 61 EYPLNERICLVGSCSTNESEKPSILVEKICISPEGDPESAVTELCIWHNLSYMKCSW 120
XX 105 EYPLNERICLVGSCSTNESEKPSILVEKICISPEGDPESAVTELCIWHNLSYMKCSW 164
XX
XX 121 LFGRTSPDTNTLYYWHRSLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
XX 165 LFGRTSPDTNTLYYWHRSLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 224
XX
XX 181 KDNAGKIKPSFNIVPLTSRVKDPDPHINKLSFHNDDLYVQWENPQNFISRCIFYEVEVNN 240
XX 225 KDNAGKIKPSFNIVPLTSRVKDPDPHINKLSFHNDDLYVQWENPQNFISRCIFYEVEVNN 284
XX
XX 241 SQTETHNVFYQEAKECPENPERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYEDDKL 300
XX 285 SQTETHNVFYQEAKECPENPERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYEDDKL 344
XX
XX 301 WSNWSQEMSIGKRNSTLYITMLIIVPVIIVAGAIL---VLLLYLKR--LKIIIPPIPD 354
XX 345 WSNWSQEMSIGKRNSTGBIE-AIVVPVCLAFLLTLLGLVLCFKNKRDLIKHHIWNVPD 403
XX
XX 355 PGK 357
XX 404 PSK 406
XX

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OM protein - protein search, using sw model

Run on: February 8, 2006, 21:59:28 ; Search time 23.7733 Seconds
(without alignments)
1622.950 Million cell updates/sec

Title: US-10-036-568A-4_COPY_26_426

Perfect score: 2172

Sequence: 1 APTEQPPVTNLSVSNELC.....QTKKETDSVVLLENKAKSQ 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*

1: Pirl:*

2: Pirl2:*

3: Pirl3:*

4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1649.5	75.9	426	2	JC7773
2	318	14.6	415	2	S12357
3	294.5	13.6	420	2	S21052
4	269.5	12.4	348	2	JC7907
5	229	10.5	335	2	A40267
6	228	10.5	400	2	S06945
7	207	9.5	373	2	A55718
8	205.5	9.5	369	2	I49280
9	202	9.3	369	2	A42565
10	197.5	9.1	831	2	J01655
11	190	8.7	610	2	A34631
12	189	8.7	310	2	A29884
13	189	8.7	412	2	A41070
14	189	8.7	610	2	A36116
15	186	8.6	581	2	I45971
16	185	8.5	616	2	A30304
17	183	8.4	292	2	I77525
18	180	8.3	303	2	I77524
19	180	8.3	608	2	I53269
20	176	8.1	630	2	I51086
21	173	8.0	918	2	A36337
22	172.5	7.9	288	2	B59405
23	172.5	7.9	376	2	A59405
24	172.5	7.9	622	2	A40144
25	170	7.8	897	1	A39255
26	165	7.6	396	2	S22909
27	163	7.5	830	2	I50455
28	162.5	7.5	333	2	S13684
29	161.5	7.4	1092	2	JX0312

interleukin-3 rece
cytokine receptor
granulocyte-macrop
interleukin-3 rece
interleukin-3 rece
interleukin-3 rece
somatotropin rece
somatotropin rece
leukemia inhibitor
glycoprotein 130 -
interleukin-6 sign
somatotropin rece
somatotropin rece
erythropoietin rec
somatotropin rece
granulocyte-macrop
interferon alpha/b

30 157 7.2 378 2 A40266
31 157 7.2 896 1 A35782
32 156.5 7.2 378 2 S50040
33 154.5 7.1 896 2 I56563
34 149 6.9 878 1 A40091
35 146.5 6.7 608 2 S32823
36 145 6.7 638 2 A33991
37 144.5 6.7 1097 2 S17308
38 144 6.6 918 2 A44257
39 142.5 6.6 917 2 I49699
40 141 6.5 638 2 S12136
41 140 6.4 638 2 B28176
42 139 6.4 508 1 ZUHUR
43 139 6.4 634 2 S33339
44 135.5 6.2 286 2 S50039
45 134.5 6.2 557 2 A32694

ALIGNMENTS

RESULT 1
JC7773
IL-13ralpha 1 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: JC7773
R:Pierrot, C.; Beniguel, L.; Beque, A.; Khalife, J.
Biochem. Biophys. Res. Commun. 287, 969-976, 2001.
A:Title: Expression of a functional IL-13ralpha by rat B cells.
A:Reference number: JC7773; PMID:11573960
A:Accession: JC7773
A:Molecule type: mRNA
A:Residues: 1-426 <PIE>
A:Cross-references: UNIPROT:Q8VHC2; UNIPARC:UPI000017CC49; GB:AY044251
C:Comment: This protein is an functionally binding protein involved in B cell proliferation
C:Genetics:
A:Gene: il-13ralpha

Query Match 75.9%; Score 1649.5; DB 2; Length 426;
Best Local Similarity 75.8%; Pred. No. 1.le-122; Indels 3; Gaps 2;
Matches 303; Conservative 43; Mismatches 51;

Qy 3 TETOPPTNLSVSVENLCTVIWTNPPGSSNCSLMYFSGDKQDKKIAPETRRSTEV 62
Db 27 TEVQPPVTNLSVSVENLCTVIWTNPPGSSNCSLMYFSGDKQDKKIAPETRRKXEL 86
Qy 63 PLNERICLVGSGQSTNESEKPSILVEKCISSPPGDPESAATELOCIWHNLSYMKCSWLP 122
Db 87 PLNEKICLVGSGQSTNESEKPSPLVKKCISSPPRGSESAVTELCQCTWHNLSYMKCSWLP 146
Qy 123 GRNTSPDNTYLYYWHRSLEKIHQECNIFREGQYFGCSFDLTVKQDSSFEQHSVQIMVKD 182
Db 147 GKNTSPDNTYLYYSSLGKSLQCNHREGHIGCSFKLTKV-ESNYEHNNIQLMKD 205
Qy 183 NAGKIPSENVPLTSRVKPPPHIKNLSFNDDLYVQWENPQNPFIISCLFYEVVNSQ 242
Db 206 NAGKIRPSYKLVSTSNVKKPPPHIKHFLKNGALFVQMKPNFESSRCLSYEVVNSTQ 265
Qy 243 TETH--NVFYVQEAECENPEFERNVENTSCFMVPGVLPTDNTNTRVKTNKLCTYEDDKL 300
Db 266 TDSYNSNLSVEEDKQCNSEFDRNMEGASCFISGVLXNTVTVVRVKTNKLCTCFDDNDL 325
Qy 301 WSNQSEMSIGKKNSTLYITMLLIVPVVAGAIIVLLYLKRLKLIIFPPPIPDGPKLPK 360
Db 326 WSNSEALSIGKEPNSTFTTMLLIIPVFVAVIIILLFYLKRLKLIIFPPPIPDGPKLPK 385
Qy 361 EMFGQNDTTLHWKKYDIYEKQTEETDSVVLLENKAKS 400
Db 386 EMFGQNDTTLHWKKYDIYEKQTEETDSVVLLENKAKA 425

RESULT 2

A:Title: Identification of an alternatively spliced isoform of the common cytokine receptor
A:Reference number: JC7907; MUID:23225486; PMID:12437989

A:Accession: JC7907

A:Molecule type: mRNA

A:Residues: 1-348 <MIN>

A:Cross-references: UNIPROT:Q8AUP2; UNIPARC:UPI00000FE604; GB:AJ419897; GB:AJ419898

A:Experimental source: egg
C:Comment: This protein, expressed as a transmembrane glycoprotein, is a novel member of
ment and proliferation.

C:Genetics:

A:Gene: ch gamma-c-a

Query Match 12.4%; Score 269.5; DB 2; Length 348;

Best Local Similarity 26.2%; Pred. No. 1e-13;

Matches 85; Conservative 60; Mismatches 125; Indels 55; Gaps 15;

Qy 93 SP-PEGDPESAVTELQCIWHNLSYMKCSWLPGRNTPSDNTYLYYHRSLEKIHCEN-I 150

Db 23 SPSPKG-----VECLFNEEYMTCTWGSQTLT--ANSLYYWYENKLPVVECCQYL 72

Qy 151 FREGYFGCSFDLTKVDDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKDPDPHIKNL 210

Db 73 WDRSVRIGRFEQSEI--IQFAFYVRVNASCGQTLEIPSNMELQNLVPEAP--VNL 128

Qy 211 SFHN---DDLVOENPQNFISRCIFYEVV--NNSQTETHNVFYQEAACENPEPERNVE 266

Db 129 TIHNSGNOLQLTWSSPY-KEQCLUEHVVKYSNODTSWTN-----QEVK----- 172

Qy 267 NTSCFMVPGVLPDLTNTVIRVTKNLCYEDDKLSNNSQEMSIGKKNST----- 317

Db 173 -GVIFSPFSDYKYYTFVRSKINNYC-GNTQLSEWSVPVFWG--NNSSTKGVAERQL 228

Qy 318 ----LYITMLLIVPVIVAGAILVLLYLKRLKIIFPIPPDPGKIFKMGDQNDTLHW 373

Db 229 QWFHTHTLPIASCLLLVLVLRMERVWIIIPRIPNPSKNFDDLFIHNGDFQEW 288

Qy 374 --KKDYIEKQTKESTDSVLIENTL 396

Db 289 VGVPKDVVSEFKPNYSESICHVSEL 313

RESULT 5

A40267

Interleukin-5 receptor alpha chain precursor - human

C:Species: Homo sapiens (man)

C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 09-Jul-2004

C:Accession: A40267

R:Tavernier, J.; Devos, R.; Cornelis, S.; Tuytens, T.; Van der Heyden, J.; Fiers, W.; Pl

Cell 66, 1175-1184, 1991

A:Title: A human high affinity interleukin-5 receptor (IL5R) is composed of an IL5-speci

A:Reference number: A40267; MUID:92005669; PMID:1833065

A:Accession: A40267

A:Molecule type: mRNA

A:Status: preliminary

A:Residues: 1-335 <TAV>

A:Cross-references: UNIPROT:Q01344; UNIPARC:UPI000002ABD4; GB:M75914; NID:g186387; PIDN:

C:Keywords: cytokine receptor; transmembrane protein

Query Match 10.5%; Score 229; DB 2; Length 335;

Best Local Similarity 24.7%; Pred. No. 1.6e-10;

Matches 82; Conservative 51; Mismatches 147; Indels 52; Gaps 14;

Qy 7 PPVTNLSVSVENLCTVIWTPN-PEGASSNCSLWYFSGDKQDKKIAPETRRSIEVPLN 65

Db 32 PPV-NFTIKVTGLAQLLQWKNPDQQRNVLEY-----QVKINAPK-EDDYETRI 82

Qy 66 ERICLQV-----GSQCSTNESEKPSILVEKCSIS-----PEGDPESAVTELQCIWHNL--- 113

Db 83 ESKCVTILHKGFSAVVRTTLQNDHSLASWSAELHAPPSPGTSIVNLCTCTTTTND 142

Qy 114 -----SY---MKCSWLPGRNTPSDNTYLYYHRSLEKIHCENIFRE--GVFGCSFDL 163

Db 143 YSLRSYQVSLHCTLWLVGDAPEDTQYFLYRYGSWTE--ECQEYSKDTLGRNIACWFFR 200

Qy 164 TKVKDSSFQHSVQIMVKDNAGKIKPSFNIVPLTSRVKDPDPHIKNLSFHNDLTVQWEN 223

Db 201 TFIILSKGRDLWSLVNGSSKHSARPPDQLPALHAIDQINPLNVTAIEGTRLSIQWEK 260

Qy 224 PON-FISRCIFYEVEVNNSTQETHNVFYQEAACENPEFERVENTSCFMVPGVLPDLN 282

Db 261 PVSAPPIHCFDYEVKIHNRNG-----YLOTEKLTNAFISIIDLSKY----- 304

Qy 283 TVRIRVTKNLCYEDDKLSNNSQEMSIGKKR 314

Db 305 DVQRAAVSSMCREAG-LWSEWSQPIYVGFSR 335

RESULT 6

S06945

granulocyte-macrophage colony-stimulating factor receptor A precursor - human

N:Alternate names: GM-CSF receptor alpha chain; hemopoietic growth factor receptor

C:Species: Homo sapiens (man)

C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004

C:Accession: S06945; A41286; A44474

R:Gearring, D.P.; King, J.A.; Gough, N.M.; Nicola, N.A.

EMBO J. 8, 3667-3676, 1989

A:Title: Expression cloning of a receptor for human granulocyte-macrophage colony-stimu

A:Reference number: S06944; MUID:90059966; PMID:2555171

A:Accession: S06945

A:Molecule type: mRNA

A:Residues: 1-400 <GEA>

R:Crosier, K.E.; Wong, G.G.; Matthey-Prevot, B.; Nathan, D.G.; Sieff, C.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 7744-7748, 1991

A:Title: A functional isoform of the human granulocyte/macrophage colony-stimulating fa

A:Reference number: A41286; MUID:91352066; PMID:1715577

A:Accession: A41286

A:Molecule type: mRNA

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Cross-references: UNIPARC:UPI0000017C141

R:Rappold, G.; Willson, T.A.; Henke, A.; Gough, N.M.

Genomics 14, 455-461, 1992

A:Title: Arrangement and localization of the human GM-CSF receptor alpha chain gene CSP.

A:Reference number: A44474; MUID:93052350; PMID:1358805

A:Accession: A44474

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 'M', 377-400 <RAP>

A:Cross-references: UNIPARC:UPI00000723FC; GB:S48539; NID:9258858; PIDN:AAB23942.1; PID

A:Note: sequence extracted from NCBI backbone (NCBIP:117980)

C:Genetics:

A:Gene: GDB:CSF2RA; CSF2R

A:Cross-references: GDB:118777; OMIM:306250; OMIM:425000

A:Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3

C:Keywords: glycoprotein; growth factor receptor; transmembrane protein

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-400/Product: granulocyte-macrophage colony-stimulating factor receptor #status pre

F:322-346/Domain: transmembrane #status predicted <TM>

F:46-54,99,123,135,182,195,223,229,272,305/Binding site: carbohydrate (Asn) (covalent)

Query Match 10.5%; Score 228; DB 2; Length 400;

Best Local Similarity 22.4%; Pred. No. 2.4e-10;

Matches 90; Conservative 82; Mismatches 180; Indels 50; Gaps 18;

Qy 5 TOPPTNLSVSVENLCTVIWTPNPEGAS-SNCSLWYFSGDKQDKKIAPETRRSIEVP 63

Db 29 TVAPASSLNVRFDSR-TMNLSDCQENTTFSCFL-----TDKNRVVEPLSNNECS 81

Qy 64 LNERICLQVGSQCSTNESEKPSILVEKCSISPEGDPESAVTELQCIWHNLSYMKCSWLPG 123

Db 82 TFEICLHEGVTFVHVNTSQRGFOQLLYPNREGRTAAQNFSCFIYNADLMNCTWARG.141

Qy 124 RNTSPDNTYLYYHRSLEKIHCENIFRE-QYFGCSFD-LTKVKDSSFQHSVQIMVK 181

Db 142 PTAPRDVQVFLYIRSKRRREIRCPYIQDSGTHVCHLDNLGLTSRNY-----FLVN 195

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QY 182 DNAGKIKPSF--NIVPLTSRVKDDPPHKNLSFHNDLLYQWENPQNF--ISRCLF-YEV 236
Db 196 GTSREIGIQFDSLLDTKTKERFNPNVNTVRCNTTHCLVRKQPRTYQKLSYLDQYQL 255
QY 237 EVN--NSQTEHNVFYVQEAACENPEPERNVENTSCFMVPGVLPDPTLNTVIRVKTNKL 294
Db 256 DVHRKKTQPTENLLINVSGLNLR-----YNFSSSPRAKSHVKIRAADVRIL 304
QY 295 YEDDKLWNWSQBSMISGKKNSS--TLYITMLLIVPVIVAGAIIVLLYLKRLKI-IIFPP 351
Db 305 N-----WSSWSEAIERFGSDNGLSVYIVLLVIGTLVCG-IVLGFLEKRFALQRLRFP 358
QY 352 IPPGKIFKMFQDN--DTLHWKXYDYE-KQTKEETDSV 390
Db 359 VPQ-----IKDKJLNDHVEDEIIWEETPEGRGYREELTV 396

RESULT 7
A55718
interleukin-2 receptor gamma chain precursor - dog
C:Species: Canis lupus familiaris (dog)
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: A55718
R:Henthorn, P.S.; Somberg, R.L.; Fimiani, V.M.; Puck, J.M.; Patterson, D.P.; Felsburg, P.
Genomics 23, 69-74, 1994
A:Title: IL-2Rgamma gene microdeletion demonstrates that canine X-linked severe combined
A:Reference number: A55718; MUID:95130114; PMID:7829104
A:Accession: A55718
A:Molecule type: mRNA
A:Status: preliminary
A:Residues: 1-373 <HEN>
A:Cross-references: UNIPROT:P40321; UNIPARC:UPI00000128CA1; GB:U04361; NID:G517411; PIDN:
C:Superfamily: interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication

Query Match 9.5%; Score 207; DB 2; Length 373;
Best Local Similarity 25.1%; Pred. No. 9.9e-09;
Matches 76; Conservative 52; Mismatches 131; Indels 44; Gaps 14;

QY 62 VPLNERICLVGSGCSTNESEKPSILVEKICSPPEGDPESAVTELOCIWHNLSYMKCSWL 121
Db 21 VGLNSTVPWNG-----NEDITDFLTATPSETLSVSSLPLEVCQFVFNVMCTWN 75
QY 122 PGRTSGPTNTYLYWHRSL--EKIHQCN-IFREGQYFCGSPDLTKVKDSSFEQHSVQI 178
Db 76 SSSEPRP-TNLTLHYWYKNSNDKQVQCGHYLFSREVTAGCW--LQKEETHLYETFFVQL 132
QY 179 MVKDNAGKIKPSNIVPLTSRVKDDPPHKNLSFHN-----DDLTVQWENPQNFISRCLFYE 235
Db 133 --RDPREPRQSTQKQLQNLVTPWAP--ENLTLHNLSEQLSLSWSN--RHLDHCLHV 186
QY 236 VEVNNSQTEHNVFYVQEAACENPEPERNVENTSCFMVPGVLPDPTLNTVIRVKTNKL 295
Db 187 VQVRSNDRSWT-----EQSDVHRNSLSPSDGQKPYTFVRVRYPNPLCG 232
QY 296 EDDKLWNWSQBSMISGK--KRNSTLYITMLLIVPVIVAGAIIVLL---LYLKLKLIIFP 350
Db 233 SAQR-WSEWHPHWGNTSKENPLFASEAVLPLGSMGLIISLICVYVWLER----SIP 287
QY 351 PIP 353
Db 288 RIP 290

RESULT 8
I49280
interleukin-2 receptor gamma chain precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C:Accession: I49280; A47514; JN0592; JN0775; S37582; I53398
R:Caio, X.; Kozak, C.A.; Liu, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993
```

```
A:Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R) ga
A:Reference number: A47514; MUID:93391374; PMID:8378320
A:Accession: I49280
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-369 <CAO>
A:Cross-references: UNIPROT:P34902; UNIPARC:UPI0000001949; EMBL:U21795; NID:G272349; PIDN:
A:Accession: A47514
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-369 <RE2>
A:Cross-references: UNIPARC:UPI0000001949; GB:L20048; NID:G404067; PIDN:AAA39286.1; PID:
R:Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamura, K.
Biochem. Biophys. Res. Commun. 193, 356-363, 1993
A:Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of functi
A:Reference number: JN0592; MUID:93277575; PMID:8503926
A:Accession: JN0592
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-369 <KUM>
A:Cross-references: UNIPARC:UPI0000001949; DDBJ:D13565; NID:G303684; PIDN:BAA02760.1; PID:
R:Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.
Gene 130, 303-304, 1993
A:Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.
A:Reference number: JN0775; MUID:93366191; PMID:8359699
A:Accession: JN0775
A:Molecule type: mRNA
A:Residues: 1-369 <ROB>
A:Cross-references: UNIPARC:UPI0000001949; GB:D13821; NID:G436045; PIDN:BAA02974.1; PID:
R:Chiu, R.K.; Dougherty, G.J.
submitted to the EMBL Data Library, October 1993
A:Description: Regulation of CD4-mediated cellular adhesion by the IL-2 R gamma chain.
A:Reference number: S37582
A:Accession: S37582
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-350, 'S', 352-366, 'S', 368-369 <CHI>
A:Cross-references: UNIPARC:UPI0000176753; EMBL:X75337
R:DiSanto, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; Avner, P.; Fischer, A.; de Sa
Eur. J. Immunol. 24, 3014-3018, 1994
A:Title: The murine interleukin-2 receptor gamma chain gene: organization, chromosomal loc
A:Reference number: I53398; MUID:95104285; PMID:7805729
A:Accession: I53398
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-369 <RES>
A:Cross-references: UNIPARC:UPI0000001949; GB:S75852; NID:G861554; PIDN:AAB32904.1; PID:
C:Genetics:
A:Gene: IL-2Rgamma
A:Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3
C:Complex: The high affinity receptor is a heterotrimer of alpha (see PIR:UHMS2), beta (f
eptors.
C:Function:
A:Description: receptor for interleukin-2
A:Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, NK ce
C:Superfamily: interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication; glycoprotein; transmembrane protein
F; 1-22/Domain: signal sequence #status predicted <SIG>
F; 23-369/Product: interleukin-2 receptor gamma chain #status predicted <MAT>
F; 256-284/Domain: transmembrane #status predicted <TMW>
F; 71,75,84,96,159,164,306/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.5%; Score 205.5; DB 2; Length 369;
Best Local Similarity 24.0%; Pred. No. 1.3e-08;
Matches 76; Conservative 63; Mismatches 121; Indels 57; Gaps 16;

QY 77 STNESEKPSILVEKICSPPEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPD---TNYT 133
Db 31 SANEDKADLLITSTAPEHLASPTLPLEVCQFVFNIEYNNCTW----NSSSPQATNLT 86
QY 134 LYVWHRSLKIHQCNIFREGQYFCGSPDLTKVKDSSFEQHSVQ-----IMVKDNAGKI 187
Db 87 LHRYKVKSD-----NNTFQCSHYLFSKEIT--SGCQIQKEDIQLYQTFVVLQDPQPKP 139
```

QY 188 KPSFNIVPLTSRVKPDPPHIKNLSFHN---DDLIVQHENPQNFISRCIFYEVEVNNQTE 244
Db 140 RRAVQKLNQNLVTPRAP--ENLTLSNLSQELRWKS-RHKIERCLQYLDVQTRSNDR 196
QY 245 THNVFYQAEKCNPEPERNVNVENTSCFVPGVLPDITLN--TVIRVTKNKLCEYEDDKLWS 302
Db 197 SWT-----ELIVNHEPRFSLPSV--DELKRYTFVRVSRVNPICGSSQ--WS 239
QY 303 NWQEMSIGK---KRNSTLYITMLLIVPVIVAGAIIVLL---YLKRLKIIIFPPIDPPG 356
Db 240 KWSQPVHWGSHVBEENSLPALEAVLIPVGTMLGIITLIFYCWLERM-----PPIP-PI 293
QY 357 KIPKEMFGDQNDITLHW 373
Db 294 KNLEDLVTEYQGNFSAW 310

RESULT 9
A:2565
interleukin-2 receptor gamma chain - human
C:Species: Homo sapiens (man)
C>Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A42565; A46591; I54332
R:Takeshita, T.; Asao, H.; Ohtani, K.; Iehii, N.; Kumaki, S.; Tanaka, N.; Munakata, H.;
Science 257, 379-382, 1992
A:Title: Cloning of the gamma chain of the human IL-2 receptor.
A:Reference number: A42565; MUID:92335883; PMID:1631559
A:Accession: A42565
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A:Residues: 1-369 <TA>
A:Cross-references: UNIPROT:P31785; UNIPARC:UPI0000000DEA; GB:D11086; NID:g303611; PIDN:
A:Experimental source: MOLT beta lymphoid cells
A:Note: sequence extracted from NCBI backbone (NCBIP:109167)
R:Nozuchi, M.; Adelstein, S.; Cao, X.; Leonard, W.J.
J. Biol. Chem. 268, 13601-13608, 1993
A:Title: Characterization of the human interleukin-2 receptor gamma chain gene.
A:Reference number: A46591; MUID:93293887; PMID:8514792
A:Accession: A46591
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RE>
A:Cross-references: UNIPARC:UPI0000000DEA; GB:L12183; NID:g307056; PIDN:AAA59145.1; PID:
R:Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Willard, H.F.; He
Hum. Mol. Genet. 2, 1099-1104, 1993
A:Title: The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-link
A:Reference number: I54332; MUID:94004847; PMID:8401490
A:Accession: I54332
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RE2>
A:Cross-references: UNIPARC:UPI0000000DEA; GB:L19546; NID:g349631; PIDN:AAC37524.1; PID:
C:Genetics:
A:Gene: GDB:IL2RG; SCIDX1; IMD4
A:Cross-references: GDB:I34807; OMIM:308380
A:Map position: Xq13.1-Xq13.1
A:Introns: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 308/3
A:Note: defects are associated with an X-linked form of severe combined immunodeficiency
C:Superfamily: interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication; immunodeficiency; transmembrane protein

Query Match 9.3%; Score 202; DB 2; Length 369;
Best Local Similarity 27.2%; Pred. No. 2.4e-08;
Matches 72; Conservative 44; Mismatches 101; Indels 48; Gaps 14;

QY 105 ELQCIWHNLSYMKCSWLPGRNTPSDTNTLYTYWHRSLEKIHQCNIFRFGQ 161
Db 59 EYQCFVFNVEYMNCTWNSSEBPQ-TNLTLYHYKNSDNKVKQKSHYLFSEITSGC-- 115
QY 162 DLTVKDSSFEQHSQVQIMVKONAGIKPSFNIVPLTSRVKPDPPHIKNLSFH--NDLLY 218
Db 116 QLOKKEIHLTYQTFVQV--QDPREPRQATQMLKQNLVIPWAP--ENLTILKLSQLE 171

QY 219 VOVENPQNFISRCI----FYEVEVNNQTEHNVFYVQAEKCNPEPERNVNVENTSCFMPV 274
Db 172 LWNVN--RFLNHCLEHLVQRTDHSWT-----EQSDVYRHKFSLP 211
QY 275 GVLPDITLVTVIRVTKNKLCEYEDDKLWSNWSQEMSIG---KRNSTLYITMLLIVPPIVA 331
Db 212 SVDGQKRYTFVRVSRFNPLC-GSAQHWSEWSPHITHGNSNTSKENPFLFALEAVVISGSM 270
QY 332 GAIIVLL---LYLKLKLIIFPPIP 353
Db 271 GLIISLLCVYFWLER-----TMRPIP 291

RESULT 10
QY1655
prolactin receptor precursor - chicken
C:Species: Gallus gallus (chicken)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JQ1655
R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA se
A:Reference number: JQ1655; MUID:93075121; PMID:1445292
A:Accession: JQ1655
A:Molecule type: mRNA
A:Residues: 1-831 <TA>
A:Cross-references: UNIPROT:Q04594; UNIPARC:UPI0000132332; DDBJ:D13154; NID:g222848; PID
A:Experimental source: Kidney
C:Keywords: glycoprotein; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-831/Product: prolactin receptor #status predicted <MAT>
F:36-219/Domain: cytokine receptor homology <CRS1>
F:239-425/Domain: cytokine receptor homology <CRS2>
F:439-462/Domain: transmembrane #status predicted <MM>
F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (coval
Query Match 9.1%; Score 197.5; DB 2; Length 831;
Best Local Similarity 23.1%; Pred. No. 1.6e-07;
Matches 91; Conservative 59; Mismatches 159; Indels 85; Gaps 19;

QY 6 QP--PVTNLSVSVENLCTV--IWT-WNPP--EGASSNCSLWYFHFQDKQKIAPEPTRR 59
Db 126 QPGSPV-NLTLETQRSANIMYLWAKWSPPLADASSN-----HLVHY-----ELRIKPEBKE 176
QY 59 SIEVPLNERICLVGSGQCTNE-----SEKPSILVEKCI 95
Db 177 EWET-----ISVGVTQCKINRLNAGMYVQVVRCTLDLPGSEWSEWSSERHILIPSGQSP 231
QY 96 EGDPESAVTELOCIWHNLSYMKCSWLPGRNTPSDTNTLYTYWHRSLEKIHQCNIFRFGQ 155
Db 232 E-----KPTIIKCSPEKETFTCWKPGLDGGHPNTYLLYSKEGEEQVYECPD-YRTAG 285
QY 156 YFGCSFDLTVKDSSFEQHSQVQIMVKONAGIKPSFNIVPLTSRVKPDPP-----HIKNL 210
Db 286 PNSCYFD--KKHTSFWTIYNTVRATNEMSGNSDPHYVDVTYIVQDPVPVNVLELKKP 343
QY 211 SFHNDLLVQVENPQNFISR-----CLFYEVEVNNQTEHNVFYVQAEKCNPEPERNVE 266
Db 344 INRKPYLVLTWSPPLADVRSGWLTLEYELRLKPEGEWETIFVGQ-QTYQKMSLN-- 400
QY 267 NTSCEFVPGVLPDITLVTVIRVTKNKLCEYEDDKLWSNWSQEMSIGKKNSTLYITMLLIV 326
Db 401 -----PGKKYIIQHKCP-----DHHGSEWSESSENYIQIPNDFRDKMIVMIV 444
QY 327 PVIAGAIIVLL---LYLKLKLIIF--PPIPDP 355
Db 445 LGVLSLLCLIMSWTMLVKGYRMITFMLPPVGP 478

RESULT 11
A34631
lactogen receptor 1 - rat

Query Match	8.6%	Score 186;	DB 2;	Length 581;
Best Local Similarity	24.3%	Pred. No. 8e-07;		
Matches	80;	Conservative 44;	Mismatches 115;	Indels 90; Gaps 16;
Qy	82	EKPSILVEKCIISPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDNTNTLYVHRSL	141	
Db	29	EKPKLV---KCRSPGK-----EFTTCWBEFGAOGGLTNTLTLYHKGE	69	
Qy	142	EKIHCENIFREGYVFGCSFDLTVKVKDSFQBHSVQIMVKDNAGAKIPKSFNIVPLTRVK	201	
Db	70	TLIHCEPD-YKTGGPNSCVF--SKGHTSIWKMYVITVNAIQMGISSDPLVYHVTVIVE	126	
Qy	202	PDPHIKVLSF---HNDD-----LYQWENPON-----FISRCLFYEVEVNSQT---E	244	
Db	127	PEPP---ANLTLELKHPEDKPKYLMIKWSPTMTDVKSGWFI---IQYERILUKPEKATDWE	181	
Qy	245	THNVFYQEAECNEPEFERNVENTSCFWPGVLPDLTMTVIRVKTNLCYEDDKLNSW	304	
Db	182	THFTLKQTKLIFN-----LYGQCKYLQIR-----CKPDPHGYNSEW	218	
Qy	305	SQEMSIGKRRNSTLYITMLLIYPVPIVAGAIIVLLLYLKLK-----IIPPPIPDPGKIF	359	

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 21:53:18 ; Search time 139,493 Seconds
(without alignments)
2028.173 Million cell updates/sec

Title: US-10-036-568A-4_COPY_26_426

Perfect score: 2172

Sequence: 1 APTETQPPVNLVSVENLC.....QTKEETDSVVLINLKASQ 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05_80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2172	100.0	427	1 I13R1_HUMAN	P78552 homo sapien
2	2172	100.0	427	2 Q5U516_XENLA	Q5U516 xenopus lae
3	2172	100.0	427	2 Q90XP8_ONCMY	Q90XP8 oncorhynchu
4	2159	99.4	426	2 Q15469_HUMAN	Q15469 homo sapien
5	2104	96.9	409	2 Q59EG2_HUMAN	P15509 homo sapien
6	1927	88.7	401	2 Q7YRV5_MACFA	Q4V311 homo sapien
7	1869	86.0	405	2 Q6U6T1_SHEEP	Q8NHV7 homo sapien
8	1859	85.6	423	2 Q5LFP1_CANFA	Q4V312 homo sapien
9	1688	77.7	424	2 Q86326_PIG	Q661N1 xenopus lae
10	1683	77.5	426	1 I13R1_MOUSE	Q76K00 sus scrofa
11	1682	77.5	424	2 Q561K3_RAT	Q8SQ71 sus scrofa
12	1682	77.0	424	2 Q8C123_MOUSE	Q86F06 rattus norv
13	1672	76.0	426	2 Q8BNM4_MOUSE	P40321 canis fami
14	1650	74.1	349	2 Q8VHC2_RAT	P34902 mus musculu
15	1387	63.9	279	2 Q9UDY5_HUMAN	Q8VHR8 rattus norv
16	977	45.0	252	2 Q8VDP7_MOUSE	
17	463	21.3	226	2 Q6ZM70_HUMAN	
18	318	14.6	415	1 ILERA_MOUSE	
19	310	14.3	386	1 I13R2_CANFA	
20	296	13.7	420	1 ILSRA_HUMAN	
21	294	13.6	380	1 I13R2_HUMAN	
22	294	13.6	420	2 Q14633_HUMAN	
23	287	13.2	383	2 Q88786_MOUSE	
24	282	13.0	396	2 Q14631_HUMAN	
25	279	12.9	415	2 Q920K4_CAVPO	
26	277	12.8	385	2 Q8VHK6_RAT	
27	273	12.6	414	2 Q920B8_RAT	
28	272	12.5	414	2 Q8VHK3_RAT	
29	269	12.4	348	2 Q8AUP2_CHICK	
30	263	12.1	391	2 Q6UAN8_TETNG	
31	262	12.1	374	2 Q8AV07_CHICK	

RESULT 1

ID	I13R1_HUMAN	STANDARD;	PRT;	427 AA.
AC	P78552	Q95646; Q99656;		
DT	01-NOV-1997	(Rel. 35, Created)		
DT	13-SEP-2005	(Rel. 48, Last sequence update)		
DE	Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-13RA-1) (CD213a1 antigen)			
GN	Name=IL13RAL; Synonyms=IL13R, IL13RA;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	TISSUE=Carcinoma;			
RC	TISSUE=SEQUENCE.			
RX	MEDLINE=97165986; PubMed=9013879; DOI=10.1016/S0014-5793(96)01462-7;			
RA	Miloux B., Laurent P., Bonnin O., Lupker J., Caput D., Vita N., Ferrara P.;			
RT	"Cloning of the human IL-13R alpha chain and reconstitution with the IL4R alpha of a functional IL-4/IL-13 receptor complex."			
RL	FEBS Lett. 401:163-166(1997).			
RN	[2]			
RP	TISSUE=B-cell;			
RC	TISSUE=SEQUENCE.			
RA	Gauchat J.F.M., Schlagenhaut E., Feng N.P., Moser R., Yamage M., Jeannin P., Alouani S., Elson G., Notarangelo L.D., Wells T., Eugster H.P., Bonnefoy J.Y.;			
RL	Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=T-cell;			
RX	MEDLINE=97067184; PubMed=8910586; DOI=10.1074/jbc.271.46.29265;			
RA	Aman M.J., Tayebi N., Obiri N.I., Puri R.K., Modi W.S., Leonard W.J.;			
RT	"cDNA cloning and characterization of the human interleukin 13 receptor alpha chain."			
RL	J. Biol. Chem. 271:29265-29270(1996).			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Wada M., Hisano T., Kuwano M.;			
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].			
RC	TISSUE=Pancreas;			
RX	MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,			

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzinski M.F., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Binds IL13 with a low affinity. Together with IL4R-alpha
 CC can form a functional receptor for IL13. Also serves as an
 CC alternate accessory protein to the common cytokine receptor gamma
 CC chain for IL4 signaling, but cannot replace the function of gamma
 CC C in allowing enhanced IL2 binding activity.
 CC -1- SUBUNIT: Interleukin 13 receptor is a complex of IL4R, IL13RA1,
 CC and possibly other components.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Ubiquitous. Highest levels in heart, liver,
 CC skeletal muscle and ovary; lowest levels in brain, lung and
 CC kidney. Also found in B-cells, T-cells and endothelial cells.
 CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding.
 CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation.
 CC -1- SIMILARITY: Belongs to the type I cytokine receptor family. Type 5
 CC subfamily.

 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

 DR ENBL; Y10659; CAA71669.1; -; mRNA.
 DR ENBL; Y09328; CAA70508.1; -; mRNA.
 DR ENBL; U62858; AAB37127.1; -; mRNA.
 DR ENBL; U81379; AAD00510.3; -; mRNA.
 DR ENBL; BC009560; AAH09560.1; -; mRNA.
 DR Ensembl; ENSG00000131724; Homo sapiens.
 DR HGNC; HGNC:5974; IL13RA1.
 DR H-InvDB; HIX0017008; -.
 DR MIM; 300119; -.
 DR GO; GO:0005898; C:interleukin-13 receptor complex; TAS.
 DR GO; GO:0005886; C:plasma membrane; TAS.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
 DR InterPro; IPR002996; Cytokn_recept_B/G.
 DR InterPro; IPR003532; Hemtptnrecept_F2.
 DR PROSITE; PS01356; HEMATOPO REC_S_F2; 1.
 KW Glycoprotein; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 427 Interleukin-13 receptor alpha-1 chain.
 FT TOPO_DOM 22 343 Extracellular (Potential).
 FT TRANSMEM 344 367 Potential.
 FT TOPO_DOM 368 427 Cytoplasmic (Potential).
 FT MOTIF 327 331 WSXWS motif.
 FT MOTIF 374 382 Box 1 motif.
 FT CARBOHYD 37 37 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 61 61 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 105 105 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 138 138 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 157 157 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 235 235 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 265 265 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 293 293 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 329 329 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 341 341 N-linked (GlcNAc. .) (Potential).
 FT DISULFID 46 95 Potential.
 FT DISULFID 134 144 By similarity.

FT DISULFID 173 185 By similarity.
 FT CONFLICT 130 130 T -> I (in Ref. 3).
 FT CONFLICT 358 358 G -> D (in Ref. 3).
 SQ SEQUENCE 427 AA; 48760 MW; 5983B3B8F554107B CRC64;
 Query Match 100.0%; Score 2172; DB 1; Length 427;
 Best Local Similarity 100.0%; Pred. No. 4.9e-158;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APTETPPVNLVSVENLCTVIWTPNPPGASNGSLWYFHFHFGDKQDKKIAPETRRSI 60
 DB 27 APTETPPVNLVSVENLCTVIWTPNPPGASNGSLWYFHFHFGDKQDKKIAPETRRSI 86
 QY 61 EVDPLNERICLOVGSQCSSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 120
 DB 87 EVDPLNERICLOVGSQCSSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 146
 QY 121 LPCRNTSPDNTYLYWHRSLKIHOCENIFRGGQVFGCSFDLTWKVDSSFEQHSVQIMV 180
 DB 147 LPCRNTSPDNTYLYWHRSLKIHOCENIFRGGQVFGCSFDLTWKVDSSFEQHSVQIMV 206
 QY 181 KONAGIKPSFNIVPLTSRVKPPPHIKNLSFNDLLYQWENPQNFISRCLFYEVVNN 240
 DB 207 KONAGIKPSFNIVPLTSRVKPPPHIKNLSFNDLLYQWENPQNFISRCLFYEVVNN 266
 QY 241 SQTETNVFVQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVTRVTKNLCYEDDKL 300
 DB 267 SQTETNVFVQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVTRVTKNLCYEDDKL 326
 QY 301 WSNWSQEMSTGKGRNSTLYITMLIIVPVIIVAGAIIVLLLYLKLKLIIRPPIIPDPGKIFK 360
 DB 327 WSNWSQEMSTGKGRNSTLYITMLIIVPVIIVAGAIIVLLLYLKLKLIIRPPIIPDPGKIFK 386
 QY 361 EMFGQNDQDTHLWKYDIYEKQTKETSDSVLLIENLKASQ 401
 DB 387 EMFGQNDQDTHLWKYDIYEKQTKETSDSVLLIENLKASQ 427
 RESULT 2
 Q5JSL4 HUMAN
 ID Q5JSL4_HUMAN PRELIMINARY; PRT; 427 AA.
 AC Q5JSL4;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Interleukin 13 receptor, alpha 1.
 GN Name=IL13RA1; ORFNames=RPL3-12804.2-001;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Lawlor S.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding (By similarity).
 CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation (By similarity).
 CC ENBL; AL391280; CAI41410.1; -; Genomic_DNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR002996; Cytokn_recept_B/G.
 DR InterPro; IPR003532; Hemtptnrecept_F2.
 DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
 KW Receptor; Transmembrane.
 SQ SEQUENCE 427 AA; 48760 MW; 5983B3B8F554107B CRC64;
 Query Match 100.0%; Score 2172; DB 2; Length 427;

Best Local Similarity 100.0%; Pred. No. 4.9e-158;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTETQPPVNLVSVENLCTVIWTPNPPGASNCSLWYFHFSGDKQDKKIAPETRISI 60
Db 27 APTETQPPVNLVSVENLCTVIWTPNPPGASNCSLWYFHFSGDKQDKKIAPETRISI 86

Qy 61 EVPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 120
Db 87 EVPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 146

Qy 121 LPGRNTSPDNTYLYWHRSLKIQHCENIFREQYFGCSFDLTWKVQSSFEQHSQVIMV 180
Db 147 LPGRNTSPDNTYLYWHRSLKIQHCENIFREQYFGCSFDLTWKVQSSFEQHSQVIMV 206

Qy 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKNLSFHNDLLYVQWENPQNFISRCCLFYEVEVNN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPDPPHINKNLSFHNDLLYVQWENPQNFISRCCLFYEVEVNN 266

Qy 241 SQTETHNVFYVOEAKCENPEPERNVENTSCFMVPGVLPDNTLVIRVKTNKLCEYEDDKL 300
Db 267 SQTETHNVFYVOEAKCENPEPERNVENTSCFMVPGVLPDNTLVIRVKTNKLCEYEDDKL 326

Qy 301 WSNWSQMSIGCKRNSTLYITMLLIVPVIVAGAIIVLLLYLKLKLIIFPPDPGKIFK 360
Db 327 WSNWSQMSIGCKRNSTLYITMLLIVPVIVAGAIIVLLLYLKLKLIIFPPDPGKIFK 386

Qy 361 EMFGDQNDTTLHWKKYDIYEKQTEEDTSVVLLENLKKASQ 401
Db 387 EMFGDQNDTTLHWKKYDIYEKQTEEDTSVVLLENLKKASQ 427

RESULT 3
ID Q96BB4 HUMAN PRELIMINARY; PRT; 427 AA.
AC Q96BB4 OSAXX08;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Interleukin 13 receptor, alpha 1,
Name=IL13RA1;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinaki M.I., Skalska U., Smallos D.E.,
RA Schnerfeld A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon;

RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
DR EMBL: BC015768; AAH15768.1; -; mRNA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .); IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR InterPro: IPR002996; Cytokn_recept_B/G.
DR InterPro: IPR003532; Hemtptnrecept_F2.
DR PROSITE: PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 427 AA; 48677 MW; 66A42F7466A39A09 CRC64;

Query Match 100.0%; Score 2172; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 4.9e-158;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTETQPPVNLVSVENLCTVIWTPNPPGASNCSLWYFHFSGDKQDKKIAPETRISI 60
Db 27 APTETQPPVNLVSVENLCTVIWTPNPPGASNCSLWYFHFSGDKQDKKIAPETRISI 86

Qy 61 EVPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 120
Db 87 EVPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 146

Qy 121 LPGRNTSPDNTYLYWHRSLKIQHCENIFREQYFGCSFDLTWKVQSSFEQHSQVIMV 180
Db 147 LPGRNTSPDNTYLYWHRSLKIQHCENIFREQYFGCSFDLTWKVQSSFEQHSQVIMV 206

Qy 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKNLSFHNDLLYVQWENPQNFISRCCLFYEVEVNN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPDPPHINKNLSFHNDLLYVQWENPQNFISRCCLFYEVEVNN 266

Qy 241 SQTETHNVFYVOEAKCENPEPERNVENTSCFMVPGVLPDNTLVIRVKTNKLCEYEDDKL 300
Db 267 SQTETHNVFYVOEAKCENPEPERNVENTSCFMVPGVLPDNTLVIRVKTNKLCEYEDDKL 326

Qy 301 WSNWSQMSIGCKRNSTLYITMLLIVPVIVAGAIIVLLLYLKLKLIIFPPDPGKIFK 360
Db 327 WSNWSQMSIGCKRNSTLYITMLLIVPVIVAGAIIVLLLYLKLKLIIFPPDPGKIFK 386

Qy 361 EMFGDQNDTTLHWKKYDIYEKQTEEDTSVVLLENLKKASQ 401
Db 387 EMFGDQNDTTLHWKKYDIYEKQTEEDTSVVLLENLKKASQ 427

RESULT 4
Q59EG2 HUMAN PRELIMINARY; PRT; 426 AA.
ID Q59EG2 HUMAN PRELIMINARY; PRT; 426 AA.
AC Q59EG2;
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE Interleukin 13 receptor, alpha 1 variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=aorta endothelial cell;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title."
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RE EMBL: AB209849; BAD93086.1; -; mRNA.


```
Db 121 LPGNTSPDNTYTLVHNSLGLQCNVIREQHIACSNLTKVKDSSFEQHSVQVMV 180
Qy 181 KDNAGKIKPSPFNIVPLTSRVKPPDPHPIKNLSFHNDLLVQWENPQNFISRCLFYEVEVNN 240
Db 181 KDNAGKIKPSPFNIVPLTSRVKPPDPHPIKNLSFQNGDLYVQWNTNPNFQSKCLSYEVEVNN 240
Qy 241 SQTETHNVFVQKACENPERNVENTSCPMVPGVLPDLTNTVIRVKTNKLCEYEDDKL 300
Db 241 SHAETHDIFVVEEAKQNTFEERLEGTICPMVPGVLPDLTNTVIRVKTNKLCEYEDDKL 300
Qy 301 WSNWSQMSIGKRNSTLYITMLLIVPVIAGAIIVLLLYLKRLLKIIIPPPIDPGKIFK 360
Db 301 WSNWSQMSIGQKAPFYITLLIIPVIAAAVILLLYLKRLLKIIIPPPIDPGKIFK 360
Qy 361 EMFGDQNDTLHWKDYIYKQTKBETDSVVLNKKASQ 401
Db 361 EMFGDQNDTLHWKDYIYKQTKBETDSVVLNKKAAQ 401

RESULT 7
ID Q95LFI_CANFA PRELIMINARY; PRT; 405 AA.
AC Q95LFI;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin 13 receptor alpha chain 1 (Fragment).
GN Name=IIL3R1;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21287533; PubMed=11389954; DOI=10.1016/S0165-2427(01)00271-9;
RA Tang L.;
RT "Molecular cloning of canine IL-13 receptor alpha chain (alpha1 and
alpha2) cDNAs and detection of corresponding mRNAs in canine
tissues."
RL Vet. Immunol. Immunopathol. 79:181-195 (2001).
DR EMBL; AF314532; AAL14886.1; -; mRNA.
DR Ensembl; ENSCARG0000018359; Canis familiaris.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytokn.recept_B/G.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003532; Hemtpnrecept_F2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor.
FT NON TER
SQ SEQUENCE 405 AA; 46328 MW; 926E1AC7BE5B3F42 CRC64;

Query Match 86.0%; Score 1869; DB 2; Length 405;
Best Local Similarity 85.5%; Pred. No. 7.8e-135;
Matches 343; Conservative 24; Mismatches 34; Indels 0; Gaps 0;

Qy 1 APTETQPPVTNLVSVENLCTVIWTNPPEGASNCNLWYFSHFQDKQDKKIAPETRISI 60
Db 5 APTETQPPVTNLVSVENLCTVIWTNPPEGASPNCTLRVYFSHFQDKQDKKIAPETRISK 64
Qy 61 EVPLNERICLVGSGCSTNESEKPSILVEKICSPPEGPESAVTELOCIWNHLSYMKCSW 120
Db 65 EVPLNERICLVGSGCSTNESEKPSILVEKICPPPEGPESAVTELOCIWNHLSYMKCTW 124
Qy 121 LPRGNTSPDNTYTLVYHRSLEKIHQCNIFREGYFGCSFDLTAKVKDSSFEQHSVQIMV 180
Db 125 LPRGNTSPDNTYTLVYHSSGLQICEDIYREGQHIQCSFALTNLKDSSFEQHSVQIMV 184
Qy 181 KDNAGKIKPSPFNIVPLTSRVKPPDPHPIKNLSFHNDLLVQWENPQNFISRCLFYEVEVNN 240
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Db 185 KDNARKIRPSPFNIVPLTSHVKPPDPHPIKRLFFQNGNLVQWKNPQNFYSRCLSYQVEVNN 244
Qy 241 SQTETHNVFVQKACENPERNVENTSCPMVPGVLPDLTNTVIRVKTNKLCEYEDDKL 300
Db 245 SQTETNDIFVVEEAKQNSFEGNLEGTICPMVPGVLPDLTNTVIRVKTNKLCEYEDDKL 304
Qy 301 WSNWSQMSIGKRNSTLYITMLLIVPVIAGAIIVLLLYLKRLLKIIIPPPIDPGKIFK 360
Db 305 WSNWSQMSIGENTDPTFYITMLLATQVIVAGAIIVLLLYLKRLLKIIIPPPIDPGKIFK 364
Qy 361 EMFGDQNDTLHWKDYIYKQTKBETDSVVLNKKASQ 401
Db 365 EMFGDQNDTLHWKDYIYKQTKBETDSVVLNKKASQ 405

RESULT 8
ID Q86326_PIG PRELIMINARY; PRT; 423 AA.
AC Q86326;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin 13 receptor alpha 1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1530752; DOI=10.1016/j.vetimm.2004.05.003;
RA Zarlega D.S.; Dawson H.; Kringel H.; Solano-Aguilar G.;
RA Urban J.F. Jr.;
RT "Molecular cloning of the Swine IL-4 receptor alpha and IL-13 receptor
1-chains: effects of experimental Toxoplasma gondii, Ascaris suum and
Trichuris suis infections on tissue mRNA levels."
RL Vet. Immunol. Immunopathol. 101:223-234 (2004).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
folding and thereby efficient intracellular transport and cell-
surface receptor binding (By similarity).
CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
activation (By similarity).
DR EMBL; AY266142; AAP23301.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytokn.recept_B/G.
DR InterPro; IPR003532; Hemtpnrecept_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 423 AA; 47984 MW; EA636FE6BCA533D9 CRC64;

Query Match 85.6%; Score 1859.5; DB 2; Length 423;
Best Local Similarity 85.0%; Pred. No. 4.4e-134;
Matches 341; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

Qy 1 APTETQPPVTNLVSVENLCTVIWTNPPEGASNCNLWYFSHFQDKQDKKIAPETRISI 60
Db 24 APAETQPPVTNLVSVENLCTVIWTNPPEGASPNCSLWYLSHFQDKQDKKIAPETRIS 83
Qy 61 EVPLNERICLVGSGCSTNESEKPSILVEKICSPPEGPESAVTELOCIWNHLSYMKCSW 120
Db 84 EVPLNERICLVGSGCSTNESEKPSILVEKICSPPEGPESAVTELOCIWNHLSYMKCTW 143
Qy 121 LPRGNTSPDNTYTLVYHRSLEKIHQCNIFREGYFGCSFDLTAKVKDSSFEQHSVQIMV 180
Db 144 LPRGNTSPDNTYTLVYHSSGLQICEDIYREGQHIQCSFALTNLKDSSFEQHSVQIMV 202
Qy 181 KDNAGKIKPSPFNIVPLTSRVKPPDPHPIKNLSFHNDLLVQWENPQNFISRCLFYEVEVNN 240
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Db 203 KDNAGKIRPAFSPVSSSHVKKPPPHIKLSFQNGDLYVQKNPQNFYSRCLSVQVEVNN 262

Qy 241 SQETETHNVFVQAKCENPFERNVENTSCFMVPGVLPDTLNTVRIRVTKNKLCEYEDDKL 300

Db 263 TQAKTHDIFVVEBAKQNSFEGNLEGMICFMVPGVLPDTLNTVRIRVTKNKLCEYEDDKL 322

Qy 301 WSNWSQMSIGKRNSTLYITMLLIVPVIVAGAILVLLYLKRLKIIIPPIPDGKIFK 360

Db 323 WSNWSQMSIGKRNSTLYITMLLIVPVIVAGAILVLLYLKRLKIIIPPIPDGKIFK 382

Qy 361 EMFGDQNDTLHWKKYDIYEKQKEETSDSVLIENLKASQ 401

Db 383 EMFGDQNDTLHWKKYDIYEKQKEETSDSVLIENLKASQ 423

RESULT 9

IL13R1 MOUSE STANDARD; PRT; 424 AA.

AC O09030; Q7TW27;

DT 01-NOV-1997 (Rel. 35, Last Created)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-13RA-1) (Interleukin-13 binding protein) (NR4).

DE 13RA-1 (Interleukin-13 binding protein) (NR4).

GN Names=IL13ral; Synonyms=IL13r, IL13ra;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidae; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RX NUCLEOTIDE SEQUENCE.

RX MEDLINE=96133964; PubMed=8552669; DOI=10.1073/pnas.93.1.497;

RA Hilton D.J., Zhang J.-G., Metcalf D., Alexander W.S., Nicola N.A., Willson T.A.;

RA "Cloning and characterization of a binding subunit of the interleukin 13 receptor that is also a component of the interleukin 4 receptor.;"

RL Proc. Natl. Acad. Sci. U.S.A. 93:497-501(1996).

RN [2]

RX NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RP STRAIN=FVB/N; TISSUE=Brain, and Colon;

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.;"

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -I- FUNCTION: Binds IL13 with a low affinity. Together with IL4R-alpha can form a functional receptor for IL13. Also serves as an alternate accessory protein to the common cytokine receptor gamma chain for IL4 signaling, but cannot replace the function of gamma C in allowing enhanced IL2 binding activity (By similarity).

CC -I- SUBUNIT: Interleukin 13 receptor is a complex of IL4R, IL13RA1, and possibly other components (By similarity).

CC -I- SUBCELLULAR LOCATION: Type I membrane protein.

CC -I- TISSUE SPECIFICITY: Spleen, liver, thymus, heart, lung, kidney, testis, stomach, brain, skin, and colon; but not skeletal muscle.

CC -I- DOMAIN: The WSXWS motif appears to be necessary for proper protein

CC folding and thereby efficient intracellular transport and cell-surface receptor binding.

CC -I- DOMAIN: The box 1 motif is required for JAK interaction and/or activation.

CC -I- SIMILARITY: Belongs to the type I cytokine receptor family. Type 5 subfamily.

CC -----

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CC -----

DR EMBL; S80963; AAB50695.1; -; mRNA.

DR EMBL; BC052425; AAB52425.2; -; mRNA.

DR EMBL; BC059939; AAB59939.1; -; mRNA.

DR Ensembl; ENSMUSG0000017057; Mus musculus.

DR MGI; MGI:105052; Il13ral.

DR GO; GO:0005615; C:extracellular space; TAS.

DR GO; GO:0016021; C:integral to membrane; TAS.

DR InterPro; IPR002996; Cytok_recept_B/G.

DR InterPro; IPR003532; Hemtptnrecept_F2.

DR PROSITE; PS01356; HEMATOPO REC S F2; 1.

KW Glycoprotein; Receptor; Signal; Transmembrane.

FT SIGNAL 1 25 Potential.

FT CHAIN 26 424 Interleukin-13 receptor alpha-1 chain.

FT TOPO_DOM 26 340 Extracellular (Potential).

FT TRANSMEM 341 364 Potential.

FT TOPO_DOM 365 424 Cytoplasmic (Potential).

FT MOTIF 324 328 WSXWS motif.

FT MOTIF 371 379 Box 1 motif.

FT CARBOHYD 35 35 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 59 59 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 103 103 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 136 136 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 262 262 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 338 338 N-linked (GlcNAc. .) (Potential).

FT DISULFID 44 93 Potential.

FT DISULFID 132 142 By similarity.

FT DISULFID 171 183 By similarity.

SQ SEQUENCE 424 AA; 48402 MW; EB8330A0DC82C9F9 CRC64;

Query Match 77.7%; Score 1688.5; DB 1; Length 424;

Best Local Similarity 77.2%; Pred. Mismatches 121;

Matches 309; Conservative 40; Gaps 1;

Qy 1 APTEPTPPVTLNLSVSVENLCTVITWNPPEGASSNLSWVFSHFGDKQKIIAPETRRSI 60

Db 25 AATEVQPPVTLNLSVSVENLCTVITWNPPEGASSNLSWVFSHFGDKQKIIAPETHRKE 84

Qy 61 EYPLNERICLVQVSGQCSSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120

Db 85 ELPLDEKICLVQVSGQCSANESKPSPLVKKICISPPGDPESAVTELCIWHNLSYMKCSW 144

Qy 121 LFGRTNTPPTNTLYYWHRSLEKIHQCEINIFREGQYFGCSFDLTVKYDSSFEQHSVQIMV 180

Db 145 LFGRTNTPPTNTLYYWHRSLEKIHQCEINIFREGQYFGCSFDLTVKYDSSFEQHSVQIMV 203

Qy 181 KDNAGKIRPESFNIVPVTSTVKPDPPIIKNLSFHNDLYVQWENPQNFISRCLEFYEVEVNN 240

Db 204 KDNAGKIRPESFNIVPVTSTVKPDPPIIKNLSFHNDLYVQWENPQNFISRCLEFYEVEVNN 263

Qy 241 SQETETHNVFVQAKCENPFERNVENTSCFMVPGVLPDTLNTVRIRVTKNKLCEYEDDKL 300

Db 264 TQAKTHDIFVVEBAKQNSFEGNLEGMICFMVPGVLPDTLNTVRIRVTKNKLCEYEDDKL 323

Qy 301 WSNWSQMSIGKRNSTLYITMLLIVPVIVAGAILVLLYLKRLKIIIPPIPDGKIFK 360

Db 324 WSDWSQAQSIGKEQNSFTFTTLLTIPVFAVAIVLLFYLLKRLKIIIPPIPDGKIFK 383

Qy 361 EMFGDQNDTLHWKKYDIYEKQKEETSDSVLIENLKAS 400

Db 384 EMFGDQNDTLHWKKYDIYEKQKEETSDSVLIENLKAS 423

RESULT 10
 Q561K3 RAT PRELIMINARY; PRT; 426 AA.
 ID AC Q561K3; DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Interleukin 13 receptor, alpha 1.
 GN Name=il13ral;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinchwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC
 RX NIH MGC Project;
 RG Submitted (APR-2005) to the EMBL/GenBank/DBSJ databases.
 RL Submitter: The WSXWS motif appears to be necessary for proper protein
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding (By similarity).
 CC -!- DOMAIN: The Box 1 motif is required for JAK interaction and/or
 CC activation (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 DR EMBL; BC093615; AAH93615.1; -; mRNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004896; C:hematopoietin/interferon-class (D200-domain. . .); IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR002996; Cytkn recept B/G.
 DR InterPro; IPR003532; Hemtptnrecept F2.
 DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
 KW Receptor; Transmembrane.
 SQ SEQUENCE 426 AA; 48464 MW; 7D2E05B7A520A8C CRC64;
 Query Match 77.5%; Score 1683.5; DB 2; Length 426;
 Best Local Similarity 77.0%; Pred. No. 1.4e-120;
 Matches 308; Conservative 43; Mismatches 46; Indels 3; Gaps 2;
 3 TTQPPVTLNLSVENVLCVTIWTWNPDPGASNCSLWYFSGDQDKKIAPETRSTRIV 62
 27 TTVQPPVTLNLSVENVLCVTIWTWNPDPGASNCSLWYFSGDQDKKIAPETRSTRIV 86
 63 PLNERICLVGSGCSTNESEKPSILVEKCISSPEGDPESAVTELOCIWNLNLSYMKCSWLP 122
 87 PLNEKICLVGSGCSTNESEKPSILVEKCISSPEGDPESAVTELOCIWNLNLSYMKCSWLP 146

123 GRNTSPDNTVTLTYWHRSLKIHQENIFREGQYFGCSFDLTVKVDSSEFQHSVQIMVKD 182
 147 GKNTSPDNTVTLTYWYSSLSGLKSLQENIHREGQHIGCSFKLTKV-ESNYEHNIIQIMVKD 205
 183 NAGKIPSFNIVPLTSRVKDDPHIKNLKSLFNDLLYQWENPQNFISRLCYEYEVNNSQ 242
 206 NAGKIRPSYKIVTSFTSNVKGPHIKHLFKNGALFQWKNPQNFSSRLCYEYEVNSTQ 265
 243 TETH--NVFVYQEAKECNPERNVENTSCFMVGLVPLDTLNTVIRVKTNKLCEVDDKL 300
 266 TDSYNSLSLEVEDKQCSFDRNNEGASCFISFGLANTVTVVRVKTNKLCEVDDNDL 325
 301 WSNWSQMSIGCKKKNSTLYITMLIIVPVIAGAILVLLYLKRLKIIFPPPIPPGKIFPK 360
 326 WSNWSEALSIGKEPNSFYITMLLIIPFVAVAVIIILLFYLKRLKIIFPPPIPPGKIFPK 385
 361 EMFGDQNDTTLHWKKYDIYEKQTEETDSVVLLENLKAA 400
 386 EMFGDQNDTTLHWKKYDIYEKQSKETDSVVLLENLKAA 425
 RESULT 11
 Q8C1Z3 MOUSE PRELIMINARY; PRT; 424 AA.
 ID Q8C1Z3; DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DE Mus musculus embryo RCB-0549 Cle-H3 cDNA, RIKEN full-length enriched
 DE library, clone:G430044106 product:interleukin 13 receptor, alpha 1,
 DE full insert sequence.
 GN Name=il13ral;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC
 RX TISSUE=Embryo;
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RT Carninci P., Hayashizaki Y.;
 RL "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC
 RX TISSUE=Embryo;
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RL "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RC The FANTOM Consortium,

[illegible]

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QY 123 GRNTSPDNTYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTQVSDSSFEQHSQIIMVKD 182
Db 147 GRNTSPDNTYLYYWSLGSLSKQOCENIHREGQHIGCSFKUTKV-ESNYEHHNIQIIMVKD 205
QY 183 NAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCILFYIEVENVNSQ 242
Db 206 NAGKIRPSYKIVSFTSNVKGPPPHIKHLFLKNGALFVQWKNPQNFSSRCLSYIEVENVSTQ 265
QY 243 TETH--NVFYVQEAACENPERNVENTSCFMVPGVLPDNTLVTRIRVKTNKLCEYEDDL 300
Db 266 TDSYNSNSLEVEDKQNSFDRNMEGASCFISPGVLANTVYTVRVKTNKLCFDDNDL 325
QY 301 WSNWSQMSIGCKNSITLYITMLIVPVIVAGAIIVLLLYLKRLLKIIIFPPIDPGKIFK 360
Db 326 WSNWSALSIGKPSNSTFYITMLLIIPFVAVVIIILLFYLKRLLKIIIFPPIDPGKIFK 385
QY 361 EMFGDQNDTLHWKKYDIYEKTEEDTSVVLLENLKKAS 400
Db 386 EMFGDQNDTLHWKKYDIYEKQSEEDTSVVLLENLKKAA 425

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DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin-13 receptor alpha-1 chain (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE
RA MEDLINE=20080132; PubMed=10614495; DOI=10.1016/S0165-2427(99)00117-8;
RX Trigona W.L., Brown W.C., Estes D.M.;
RT "Functional implications for signaling via the IL4R/IL13R complex on
   bovine cells.";
RL Vet. Immunopathol. 72:73-79(1999).
DR EMBL; AF074402; AAC98147.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytokn_recept B/G.
DR InterPro; IPR003532; Hemtptnrecept F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 349 349
SQ SEQUENCE 349 AA; 39644 MW; D61A4C918B1940A6 CRC64;

Query Match 74.18; Score 1610; DB 2; Length 349;
Best Local Similarity 84.5%; Pred. No. 4.6e-115;
Matches 295; Conservative 17; Mismatches 37; Indels 0; Gaps 0;

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Db 1 VTNLVSVENLCTIITWTWNPPEGASPNCSLKYFSHFGNKGDKKIAPETHRSKEVPLNERI 60
QY 69 CLQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSWI PGRNTSP 128
Db 61 CLQVGSQCSTNESEKPSILVEKICISPPGDPESAVTALQCIWHNLR YMKCTWLPGRNASP 120
QY 129 DTNYTLTYWHRSLEKIHOCENIFREGQYFGCSFDLTQVSDSSFEQHSQIIMVKDAGKIK 188
Db 121 DPNTILTYWNSLGIKIQCFNFRYEGQHIACSFNLTQVSDSSFEQHSQVQWVRDNAGKIS 180
QY 189 PSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCILFYIEVENVNSQETHVY 248
Db 181 PSFNIVPLTSRVKPPPHIKNLSFQNGDLYVQWTFNPNFQSQCLCYIEVEVINSHAEHDI 240
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Db 241 FYVQEAACQNTPEGNLEGICFMVPGVLPDNTLVTRIRVKTNKLCEYEDDLKSNWSQAM 300
QY 309 SIGCKRNSITLYITMLIVPVIVAGAIIVLLLYLKRLLKIIIFPPIDPGK 357
Db 301 SIGQKANTFYITLLIIPVIVAAVIVLLLYLKRLLKIIIFPPIDPGK 349

RESULT 15
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AC O9UDY5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Interleukin-13 receptor soluble form (Interleukin 13 receptor, alpha
   1).
GN Name=IL13RA1; ORFNames=RP13-12804.2-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wada M., Hisano T., Kuwano M.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lawlor S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
   folding and thereby efficient intracellular transport and cell-
   surface receptor binding (By similarity).
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
   activation (By similarity).
DR EMBL; U81380; AAC00511.2; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytokn_recept B/G.
DR InterPro; IPR003532; Hemtptnrecept F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 279 AA; 31659 MW; E74141F99F8E9EBB CRC64;

Query Match 63.9%; Score 1387; DB 2; Length 279;
Best Local Similarity 99.6%; Pred. No. 4.4e-98;
Matches 251; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 27 APTETQPPVTNLVSVENLCTIWTWNPPEGASNCSLWYFSHFGDKQDKKIAPETRRI 86
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Db 87 EVPLNERICLQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 146
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Db 147 LPGRNTSPDNTYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTQVSDSSFEQHSQIIMV 206
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCILFYIEVENV 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCILFYIEVENV 266
QY 241 SQETHNVFYVQ 252
Db 267 SQETHNVFVTR 278
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

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(without alignments)
998.200 Million cell updates/sec

Title: US-10-036-568A-4_COPY_26_426

Perfect score: 2172
Sequence: 1 APTETQPPVTNLSVSNLC.....QTKEETDSVVLNKKASQ 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgm2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgm2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
5: /cgm2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2172	100.0	426	2	US-09-688-286D-4
2	2172	100.0	427	2	US-08-969-125-9
3	2172	100.0	427	2	US-09-545-002-9
4	2172	100.0	427	2	US-09-949-016-6094
5	1869	86.0	405	2	US-09-828-995B-50
6	1749.5	80.5	784	2	US-09-313-942-30
7	1749.5	80.5	784	2	US-10-282-162-30
8	1745	80.3	322	2	US-09-825-561A-82
9	1745	80.3	793	2	US-09-313-942-32
10	1745	80.3	793	2	US-10-282-162-32
11	1688.5	77.7	424	2	US-09-688-286D-2
12	1265	58.2	233	2	US-09-949-016-8550
13	318	14.6	398	1	US-07-757-390-6
14	318	14.6	398	1	US-08-442-282-6
15	318	14.6	398	1	US-08-442-281-6
16	318	14.6	398	1	US-08-939-727-6
17	318	14.6	415	1	US-07-757-390-5
18	318	14.6	415	1	US-08-442-282-5
19	318	14.6	415	1	US-08-442-281-5
20	318	14.6	415	1	US-08-939-727-5
21	318	14.6	415	2	US-09-886-319A-23
22	310	14.3	365	2	US-09-828-995B-66
23	310	14.3	386	2	US-09-828-995B-61
24	304.5	14.0	561	2	US-09-828-995B-72
25	303.5	14.0	561	2	US-09-828-995B-81
26	297	13.7	565	2	US-09-828-995B-75
27	296.5	13.7	420	2	US-09-886-319A-24

28	296.5	13.7	420	2	US-09-949-016-5958	Sequence 5958, Ap
29	296	13.6	318	2	US-09-828-995B-69	Sequence 69, Appl
30	296	13.6	563	2	US-09-828-995B-78	Sequence 78, Appl
31	294.5	13.6	380	1	US-08-609-572-4	Sequence 4, Appli
32	294.5	13.6	380	2	US-08-841-751-4	Sequence 4, Appli
33	294.5	13.6	380	2	US-08-846-340-4	Sequence 4, Appli
34	294.5	13.6	380	2	US-08-846-344-4	Sequence 4, Appli
35	294.5	13.6	380	2	US-09-301-808-4	Sequence 13, Appl
36	294.5	13.6	420	1	US-07-757-390-13	Sequence 13, Appl
37	294.5	13.6	420	1	US-08-442-282-13	Sequence 13, Appl
38	294.5	13.6	420	1	US-08-442-281-13	Sequence 13, Appl
39	294.5	13.6	420	1	US-08-939-727-13	Sequence 13, Appl
40	293.5	13.5	427	2	US-09-949-016-8614	Sequence 8614, Ap
41	293.5	13.5	427	2	US-09-949-016-8620	Sequence 8620, Ap
42	287.5	13.2	383	1	US-08-609-572-2	Sequence 2, Appli
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ALIGNMENTS

RESULT 1

US-09-688-286D-4
; Sequence 4, Application US/09688286D
; Patent No. 6911530
; GENERAL INFORMATION:
; APPLICANT: Willson, Tracey
; APPLICANT: Nicola, Nicos
; APPLICANT: Hilton, Douglas
; APPLICANT: Metcalf, Donald
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: A novel haemopoietin receptor and genetic sequences encoding same
; FILE REFERENCE: 23199-215
; CURRENT APPLICATION NUMBER: US/09/688,286D
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: AU PN6135
; PRIOR FILING DATE: 1995-10-23
; PRIOR APPLICATION NUMBER: AU PN7276
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: AU PP2208
; PRIOR FILING DATE: 1996-09-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 426
; TYPE: PRT
; ORGANISM: human
US-09-688-286D-4

Query Match	100.0%	Score 2172;	DB 2;	Length 426;			
Best Local Similarity	100.0%	Pred. No. 6.4e-212;					
Matches 401;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0			
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Db	146	LPGRNTSPDNTY	TYLWYHRSLEKIHQ	CENIFREG	QYFC	SDPDKTKVQSSPFOHSVQIMV 205	
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Db	206	KDNAGKIKPSFN	IVPLTSRVKPD	PHIKNLS	PHND	LYVQ	MENPNQFISRCIFYEVEVNN 265
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Db 326 WSNWSQMSIGKGRNSTLYITMLLIYPVIVAGAIIVLLLYLKLKLIIFPPIDPGKIFK 385
QY 361 EMFGDQNDTLHWKXYDIYEKQTKETSDSVLIENLKASQ 401
Db 386 EMFGDQNDTLHWKXYDIYEKQTKETSDSVLIENLKASQ 426

RESULT 2
US-08-969-125-9
; Sequence 9, Application US/08969125B
; Patent No. 6143871
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, JEAN-YVES
; GAUCHAT, JEAN-FRANCOIS
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,125B
; FILING DATE: 12-No. 6143871-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9625899.1
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 427 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-969-125-9

Query Match 100.0%; Score 2172; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 6.4e-212;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTEPTOPPVTNLVSVENLCTVIWTWNPPEGASNSCLWYFHFHFGDKQDKKIAPETRRSI 60
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Db 207 KONAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDDLYVQWENPQNFISRCLFYEVEVNN 266
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Db 267 SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVTRIRVKTNKLKYEDDKL 326
QY 301 WSNWSQMSIGKGRNSTLYITMLLIYPVIVAGAIIVLLLYLKLKLIIFPPIDPGKIFK 360
Db 327 WSNWSQMSIGKGRNSTLYITMLLIYPVIVAGAIIVLLLYLKLKLIIFPPIDPGKIFK 386
QY 361 EMFGDQNDTLHWKXYDIYEKQTKETSDSVLIENLKASQ 401
Db 387 EMFGDQNDTLHWKXYDIYEKQTKETSDSVLIENLKASQ 427

RESULT 3
US-09-545-002-9
; Sequence 9, Application US/09545002
; Patent No. 6743604
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, JEAN-YVES
; GAUCHAT, JEAN-FRANCOIS
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/545,002
; FILING DATE: 12-No. 6743604-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,125
; FILING DATE: 12-No. 6743604-1997
; APPLICATION NUMBER: GB 9625899.1
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 427 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-545-002-9

Query Match 100.0%; Score 2172; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 6.4e-212;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTEPTOPPVTNLVSVENLCTVIWTWNPPEGASNSCLWYFHFHFGDKQDKKIAPETRRSI 60
Db 27 APTEPTOPPVTNLVSVENLCTVIWTWNPPEGASNSCLWYFHFHFGDKQDKKIAPETRRSI 86
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Db 147 LPGRNTSPDNTLYTYWHSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 206
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Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFSRCLFYVEVNN 266
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Db 267 SQTETHNVFYVQEAACENPEERNVENTSCFMVPGVLPDNTLVIRVTKNKLCEYDDKL 326
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Db 327 WSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLYLKRLKIIFFPPDPGKIFK 386
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Db 387 EMFGDQNDTTLHWKDYIYEKQTKETSDSVVLIENLKASQ 427
RESULT 4
US-09-949-016-6094
; Sequence 6094, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6094
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6094
Query Match 100.0%; Score 2172; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 6.4e-212; Indels 0; Gaps 0;
Matches 401; Conservative 0; Mismatches 0
Qy 1 APTETQPPVTNLSVSVENLCTVIWTPNPPGASNCSLWYFSHFGDKQDKKIAPETRRSI 60
Db 27 APTETQPPVTNLSVSVENLCTVIWTPNPPGASNCSLWYFSHFGDKQDKKIAPETRRSI 86
Qy 61 EVPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPESAVTELOCIMWNLKSCSW 120
Db 87 EVPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPESAVTELOCIMWNLKSCSW 146
Qy 121 LPGRNTSPDNTLYTYWHSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
Db 147 LPGRNTSPDNTLYTYWHSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 206
Qy 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFSRCLFYVEVNN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFSRCLFYVEVNN 266
Qy 241 SQTETHNVFYVQEAACENPEERNVENTSCFMVPGVLPDNTLVIRVTKNKLCEYDDKL 300
Db 267 SQTETHNVFYVQEAACENPEERNVENTSCFMVPGVLPDNTLVIRVTKNKLCEYDDKL 326
Qy 301 WSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLYLKRLKIIFFPPDPGKIFK 360
Db 327 WSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLYLKRLKIIFFPPDPGKIFK 386

Qy 361 EMFGDQNDTTLHWKDYIYEKQTKETSDSVVLIENLKASQ 401
Db 387 EMFGDQNDTTLHWKDYIYEKQTKETSDSVVLIENLKASQ 427
RESULT 5
US-09-828-995B-50
; Sequence 50, Application US/09828995B
; Patent No. 6703360
; GENERAL INFORMATION:
; APPLICANT: Heska Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13 R
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/09/828,995B
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-828-995B-50
Query Match 86.0%; Score 1869; DB 2; Length 405;
Best Local Similarity 85.5%; Pred. No. 3.7e-181;
Matches 343; Conservative 24; Mismatches 34; Indels 0; Gaps 0;
Qy 1 APTETQPPVTNLSVSVENLCTVIWTPNPPGASNCSLWYFSHFGDKQDKKIAPETRRSI 60
Db 5 APTETQPPVTNLSVSVENLCTVIWTPNPPGASNCSLWYFSHFGDKQDKKIAPETRRSI 64
Qy 61 EVPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPESAVTELOCIMWNLKSCSW 120
Db 65 EVPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPESAVTELOCIMWNLKSCSW 124
Qy 121 LPGRNTSPDNTLYTYWHSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
Db 125 LPGRNTSPDNTLYTYWHSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 184
Qy 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFSRCLFYVEVNN 240
Db 185 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFSRCLFYVEVNN 244
Qy 241 SQTETHNVFYVQEAACENPEERNVENTSCFMVPGVLPDNTLVIRVTKNKLCEYDDKL 300
Db 245 SQTETHNVFYVQEAACENPEERNVENTSCFMVPGVLPDNTLVIRVTKNKLCEYDDKL 304
Qy 301 WSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLYLKRLKIIFFPPDPGKIFK 360
Db 305 WSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLYLKRLKIIFFPPDPGKIFK 364
Qy 361 EMFGDQNDTTLHWKDYIYEKQTKETSDSVVLIENLKASQ 401
Db 365 EMFGDQNDTTLHWKDYIYEKQTKETSDSVVLIENLKASQ 405
RESULT 6
US-09-313-942-30
; Sequence 30, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: RECEPTOR AND USING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942

```
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-30

Query Match      80.5%; Score 1749.5; DB 2; Length 784;
Best Local Similarity 90.5%; Pred. No. 1.4e-168;
Matches 323; Conservative 5; Mismatches 14; Indels 15; Gaps 2;

Qy 1 APTETQPPVNLVSVENLCTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 60
Db 239 APTETQPPVNLVSVENLCTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 238
Qy 61 EVPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPDESATVTELCIWHNLSYMKCSW 120
Db 299 EVPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPDESATVTELCIWHNLSYMKCSW 358
Qy 121 LPRGNTSPDNTNLTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFEGHVSQIMV 180
Db 359 LPRGNTSPDNTNLTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFEGHVSQIMV 418
Qy 181 KDNAGKIKPSFNIVPLTSRVKDPDPHINKLSFNHDDLIVQWENPQNFISRCCLFYEVVNN 240
Db 419 KDNAGKIKPSFNIVPLTSRVKDPDPHINKLSFNHDDLIVQWENPQNFISRCCLFYEVVNN 478
Qy 241 SQTETHNVFVQEAACENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLKYEDDKL 300
Db 479 SQTETHNVFVQEAACENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLKYEDDKL 538
Qy 301 WSNWSQEMSIGKGRNST-----LYITMLLIVPVIVAGAIIVLLLYLRLKLIIPPPIP 353
Db 539 WSNWSQEMSIGKGRNSTTGDKTHTCCPAPPELLGGP-----SVFLFPPKP 584

RESULT 7
US-10-282-162-30
; Sequence 30, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR FILING DATE: 1999-09-22
; PRIOR FILING DATE: 1999-09-22
; PRIOR FILING DATE: 1999-09-22
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-30

Query Match      80.5%; Score 1749.5; DB 2; Length 784;
Best Local Similarity 90.5%; Pred. No. 1.4e-168;
Matches 323; Conservative 5; Mismatches 14; Indels 15; Gaps 2;

Qy 1 APTETQPPVNLVSVENLCTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 60
Db 239 APTETQPPVNLVSVENLCTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 238
Qy 61 EVPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPDESATVTELCIWHNLSYMKCSW 120
Db 299 EVPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPDESATVTELCIWHNLSYMKCSW 358
Qy 121 LPRGNTSPDNTNLTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFEGHVSQIMV 180
Db 359 LPRGNTSPDNTNLTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFEGHVSQIMV 418
Qy 181 KDNAGKIKPSFNIVPLTSRVKDPDPHINKLSFNHDDLIVQWENPQNFISRCCLFYEVVNN 240
Db 419 KDNAGKIKPSFNIVPLTSRVKDPDPHINKLSFNHDDLIVQWENPQNFISRCCLFYEVVNN 478
Qy 241 SQTETHNVFVQEAACENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLKYEDDKL 300
Db 479 SQTETHNVFVQEAACENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLKYEDDKL 538
Qy 301 WSNWSQEMSIGKGRNST-----LYITMLLIVPVIVAGAIIVLLLYLRLKLIIPPPIP 353
Db 539 WSNWSQEMSIGKGRNSTTGDKTHTCCPAPPELLGGP-----SVFLFPPKP 584

RESULT 8
US-09-825-561A-82
; Sequence 82, Application US/09825561A
; Patent No. 6777539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. 6777539ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Neilson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR FILING DATE: 2000-04-05
; PRIOR FILING DATE: 2000-04-05
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-82

Query Match      80.3%; Score 1745; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-168;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTETQPPVNLVSVENLCTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 60
Db 6 APTETQPPVNLVSVENLCTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 65
Qy 61 EVPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPDESATVTELCIWHNLSYMKCSW 120
Db 66 EVPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPDESATVTELCIWHNLSYMKCSW 125
Qy 121 LPRGNTSPDNTNLTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFEGHVSQIMV 180
Db 126 LPRGNTSPDNTNLTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFEGHVSQIMV 185
Qy 181 KDNAGKIKPSFNIVPLTSRVKDPDPHINKLSFNHDDLIVQWENPQNFISRCCLFYEVVNN 240
Db 186 KDNAGKIKPSFNIVPLTSRVKDPDPHINKLSFNHDDLIVQWENPQNFISRCCLFYEVVNN 245
Qy 241 SQTETHNVFVQEAACENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLKYEDDKL 300
Db 246 SQTETHNVFVQEAACENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLKYEDDKL 305
Qy 301 WSNWSQEMSIGKGRNST 317
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; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-32

Query Match      80.3%; Score 1745; DB 2; Length 793;
Best Local Similarity 100.0%; Pred. No. 4.le-168;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTETQPPVNLVSVENLCTVTWTWNPPEGASNCSLWYFSHFGQDKKIAPIETRRI 60
    |||
Db 27 APTETQPPVNLVSVENLCTVTWTWNPPEGASNCSLWYFSHFGQDKKIAPIETRRI 86
    |||

Qy 61 EVPLNERICIQVGSQCSTNSEKPSILVEKCIIPPEGDPESA TELQCIWHNLSYMKCSW 120
    |||
Db 87 EVPLNERICIQVGSQCSTNSEKPSILVEKCIIPPEGDPESA TELQCIWHNLSYMKCSW 146
    |||

Qy 121 LPGRNTSPDNTYTLYYWHRSLKIHQENIFRSGQYFGCSFDLTWKVXDSSFQHSVQIMV 180
    |||
Db 147 LPGRNTSPDNTYTLYYWHRSLKIHQENIFRSGQYFGCSFDLTWKVXDSSFQHSVQIMV 206
    |||

Qy 181 KDNAGKIKPSFNIVPLTSRVKPPDPPIKNI SFHNDLLYQWENPQNFI SRCLFYFEVENVN 240
    |||
Db 207 KDNAGKIKPSFNIVPLTSRVKPPDPPIKNI SFHNDLLYQWENPQNFI SRCLFYFEVENVN 266
    |||

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[illegible][illegible]

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Db      85  ELPLDEKICLVGSCQSANESKPSPLVKKICSPPEGDPESAVTELKCIWHNLSYMKCSW 144
Qy      121  LPGNTSPDNTYLYYHRSLEKIHQCNIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
Db      145  LPGNTSPDTHYLYYWSLSKSRQCENIYREGQHIACSFKLTKV-EPSFEHQNVQIMV 203
Qy      181  KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLLVQWENPQNFIISCLFYEVEVNN 240
Db      204  KDNAGKIRPCKIVSLTSYVKPDPPHIKHLKLLKNGALLVQWKPNQPNFRSCLTYEVEVNN 263
Qy      241  SQETHNVFVQEAACENPFRNVENTSCFMVPGVLPDTLNTRIRVKTNKLCEYDDKL 300
Db      264  TQTDHNLVEEDKQCNSSDRNMGTSFQLPGVLADAVYTVRVKTNKLCFDDNKL 323
Qy      301  WSNWSQEMSGKKRNSTLYTMLIVPVIIVAGAIIVLLLYLKRKLIIFPPIDPDGKIFK 360
Db      324  WSDWSEASQSIGKEQNSTFYTTMLITIPFVAVAVIILLFYLKRLKIIFPPIDPDGKIFK 383
Qy      361  EMFGDQNDTLHWKKYDIYEKOTKEETDSVLIENLKAS 400
Db      384  EMFGDQNDTLHWKKYDIYBKQSBETDSVLIENLKAA 423

RESULT 12
US-09-949-016-8550
; Sequence 8550, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 8550
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8550

Query Match      58.2%; Score 1265; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 3.8e-120;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      51  KIAPETRRSIEVPLNERICLVGSCQSTNESEKPSILVEKCIIPPEGDPESAVTELCQIW 110
Db      1  KIAPETRRSIEVPLNERICLVGSCQSTNESEKPSILVEKCIIPPEGDPESAVTELCQIW 60

Qy      111  HNLSYMKCSWLPGRNTSPDNTYLYYHRSLEKIHQCNIFREGQYFGCSFDLTWKVDSS 170
Db      61  HNLSYMKCSWLPGRNTSPDNTYLYYHRSLEKIHQCNIFREGQYFGCSFDLTWKVDSS 120

Qy      171  FEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLLVQWENPQNFI 230
Db      121  FEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLLVQWENPQNFI 180

Qy      231  CLFYEVEVNNQSQTETHNVFVQEAACENPFRNVENTSCFMVPGVLPDTL 281
Db      181  CLFYEVEVNNQSQTETHNVFVQEAACENPFRNVENTSCFMVPGVLPDTL 231
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RESULT 13
US-07-757-390-6
; Sequence 6, Application US/07757390
; Patent No. 5453491
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; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/757,390
; FILING DATE: 19910910
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-757-390-6

Query Match      14.6%; Score 318; DB 1; Length 398;
Best Local Similarity 23.9%; Pred. No. 1.5e-23;
Matches 97; Conservative 74; Mismatches 179; Indels 56; Gaps 14;

Qy      7  PPVTNLSVSVENLCTVIWTWNP-PGASNSCSLWYFSHP-GDKQDKKIAPETRRSIEVPL 64
Db      12  PPV-NFTIKATGLAQVLLHWDPNPQQRHVDLEYHVKINAPQEDBYDTRKTESKCVTPL 70

Qy      65  NERICLVGSCQSTNESEKPSILVEKCIIPPEGDPESAVTELCQIWHNL----- 113
Db      71  HEGFAASVRTLKSSHTTLASSWVSAELKAPPGSGTSTNLTCTTHTTVVSSHTRLRPYQ 130

Qy      114  SYMKCSWLPGRNTSPDNTYLYYHRSLEKIHQCNIFRE--GQYFGCSFDLTWKVDSSF 171
Db      131  VSLRCTLWKGDAPEDTQYFLYRFGVLTE--KCQYSRDALNRNTACWPRTFINSKGF 198

Qy      172  EQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLLVQWENPQN-FISR 230
Db      189  EQLAVHINGSKRAAIKPPDQLFSLAIDQVNPNNVTVEIESNLSLYIQWEKPLSAPPDH 248

Qy      231  CLFYEVEVNNQSQTETHNVFVQEAACENPFRNVENTSCFMVPGVLPDTLNTRIRVKT 290
Db      249  CFNYELKIYNTKNG-----HIQKEKLIANKFISKIDDVSTY-----SIQVRAAV 292

Qy      291  NKLCEYBDDKLSWSQEMSGKKRNSTLYTMLIVPVIIVAGAIIVLLLYLKRKLI--- 347
Db      293  SSFCRMPGR-WGWSQPIYVGERKS-LVENHLIVLP---TAACFVLLIFSLICRVCHLW 347

Qy      348  --IFPPIDPDGKIKFEMFGDQNDTLHWKKYDIYEKOTKEETDSV 391
Db      348  TRLFPVPVPAPKSNIKDL-----PVTVEYKPSNETKIEV 382
```

RESULT 14
US-08-442-282-6
; Sequence 6, Application US/08442282
; Patent No. 5760204
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,282
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Lealie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-442-282-6

Query Match 14.6%; Score 318; DB 1; Length 398;
Best Local Similarity 23.9%; Pred. No. 1.5e-23;
Matches 97; Conservative 74; Mismatches 179; Indels 56; Gaps 14;
QY 7 PPVTNLSVSVENLCTVIWTPN-PEGASNSCLWYFSHP-GDKQDKKIAPETRRSIEVPL 64
DB 12 PPV-NFTIKATGLAQVLLHWDNPQEQRHVDLEYHVKNAPQDEYDTRKTESKCVTPL 70
QY 65 NERICLVGSCQSTNESEKPSILVEKCI-SPPEGDPESAVTELOCIWHNL----- 113
DB 71 HEGFAASVRTILKSHHTTLASSWSVAELKAPPGSGTSTVNLCTTHTVSSHTLHPYQ 130
QY 114 SYMKCSWLPGRNTSPDNTYLYMHRSLKIHQCENIFRE--GOYFGCSFDLTVKVDSF 171
DB 131 VSLRCTLVGGKADPDTQYFLYRFGVLTE--KCQEYSDALNRNTACWFPRTFINSKGF 188
QY 172 EQHSVQIMVKONAGKIKPSFNIVPLTSRVKDPDPHINKLSFNHDDLTVQWENPQN-FISR 230
DB 189 EQLAVHINGSSKRAAIKPFQDLFSLAIDQVNPVRNVTVEIESLSLIQWKPFLSAFPDH 248
QY 231 CLFYEYVNNSTQETNNVYQAEKCNENPFRNVENTSCFVMPGVLPDTLNVTIRVKT 290
DB 249 CFNYELKIYNTKNG-----HIQEKELIANKFISKIDVSTY-----SIQVRAV 292
QY 291 NKLCEYDDKLNWNSGEMSIGKRNSTLYITMLLIVPVIVACAIIVLLILLYLKLKLI--- 347

DB 293 SSFCRMPGR-WGEWSQPIYVGKERS-LVEMHLIVLP---TAACFVLLIFSLICRVCHLM 347
QY 348 --IFPPIDPGKIFKEMFGQNDTTLHWKKYDIYEKQKEETDSVV 391
DB 348 TRLFPVPVAPKSNKDL-----PVVTEYEKPSNETKIEVV 382
RESULT 15
US-08-442-281-6
; Sequence 6, Application US/08442281
; Patent No. 5807991
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,281
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Lealie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-442-281-6
Query Match 14.6%; Score 318; DB 1; Length 398;
Best Local Similarity 23.9%; Pred. No. 1.5e-23;
Matches 97; Conservative 74; Mismatches 179; Indels 56; Gaps 14;
QY 7 PPVTNLSVSVENLCTVIWTPN-PEGASNSCLWYFSHP-GDKQDKKIAPETRRSIEVPL 64
DB 12 PPV-NFTIKATGLAQVLLHWDNPQEQRHVDLEYHVKNAPQDEYDTRKTESKCVTPL 70
QY 65 NERICLVGSCQSTNESEKPSILVEKCI-SPPEGDPESAVTELOCIWHNL----- 113
DB 71 HEGFAASVRTILKSHHTTLASSWSVAELKAPPGSGTSTVNLCTTHTVSSHTLHPYQ 130
QY 114 SYMKCSWLPGRNTSPDNTYLYMHRSLKIHQCENIFRE--GOYFGCSFDLTVKVDSF 171
DB 131 VSLRCTLVGGKADPDTQYFLYRFGVLTE--KCQEYSDALNRNTACWFPRTFINSKGF 188
QY 172 EQHSVQIMVKONAGKIKPSFNIVPLTSRVKDPDPHINKLSFNHDDLTVQWENPQN-FISR 230
DB 189 EQLAVHINGSSKRAAIKPFQDLFSLAIDQVNPVRNVTVEIESLSLIQWKPFLSAFPDH 248

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 22:28:54 ; Search time 108.728 Seconds
(without alignments)
1540.998 Million cell updates/sec

Title: US-10-036-568A-4_COPY_26_426

Perfect score: 2172
Sequence: 1 APTETQPPVTNLSVSVENLCTVITWNPPEGAGNCNLSLWYFSGDKODKKIAPETRRSI 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp:*
2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp:*
3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp:*
4: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp:*
5: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp:*
6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2172	100.0	427	4	US-10-671-697-9
2	2172	100.0	427	6	US-11-067-251-3
3	2165	99.7	427	5	US-10-850-270-4
4	2154	99.2	426	4	US-10-036-568-4
5	1869	86.0	405	3	US-09-828-995B-50
6	1869	86.0	405	4	US-10-753-159-50
7	1784.5	82.2	664	5	US-10-850-270-10
8	1750	80.6	776	3	US-09-935-868-36
9	1749.5	80.5	784	3	US-09-313-942-30
10	1749.5	80.5	784	3	US-09-935-868-30
11	1749.5	80.5	784	4	US-10-287-035-30
12	1749.5	80.5	784	4	US-10-282-162-30
13	1749.5	80.5	784	6	US-11-134-114-30
14	1745	80.3	322	3	US-09-825-561A-82
15	1745	80.3	322	5	US-10-872-087-82
16	1745	80.3	322	3	US-09-935-868-34
17	1745	80.3	793	3	US-09-313-942-32
18	1745	80.3	793	3	US-09-935-868-32
19	1745	80.3	793	4	US-10-287-035-32
20	1745	80.3	793	4	US-10-282-162-32
21	1745	80.3	793	6	US-11-134-114-32
22	1741	80.2	776	3	US-09-935-868-44
23	1741	80.2	776	4	US-10-287-035-40
24	1741	80.2	776	6	US-11-067-251-8
25	1741	80.2	776	6	US-11-067-251-10
26	1741	80.2	776	6	US-11-067-251-12
27	1741	80.2	776	6	US-11-067-251-14

ALIGNMENTS

RESULT 1

US-10-671-697-9

Sequence 9, Application US/10671697

Publication No. US20040043921A1

GENERAL INFORMATION:

APPLICANT: BONNEFOY, JEAN-YVES

GAUCHAT, JEAN-FRANCOIS

TITLE OF INVENTION: SUBSTANCES AND THEIR USES

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHUYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/671,697

FILING DATE: 29-Sep-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/545,002

FILING DATE: 06-APR-2000

APPLICATION NUMBER: US 08/969,125

FILING DATE: 12-NOV-1997

APPLICATION NUMBER: GB 9625899.1

FILING DATE: 13-DEC-1996

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 427 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-10-671-697-9

Query Match 100.0%; Score 2172; DB 4; Length 427;

Best Local Similarity 100.0%; Pred. No. 7.8e-180;

Mismatches 0; Indels 0; Gaps 0;

Matches 401; Conservative

Qy	1	APTETQPPVTNLSVSVENLCTVITWNPPEGAGNCNLSLWYFSGDKODKKIAPETRRSI	60
Db	27	APTETQPPVTNLSVSVENLCTVITWNPPEGAGNCNLSLWYFSGDKODKKIAPETRRSI	86
Qy	61	EVLPLNERICLVGSCSTNESEKPSILVKEKICISPPGDPESAVTELCQIWHNLSYMKCSW	120

Db 87 EVPLNERICLVGSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 146
Qy 121 LPRGNTSPDNTYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 180
Db 147 LPRGNTSPDNTYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 206
Qy 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNFISRCLFYEVVNN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNFISRCLFYEVVNN 266
Qy 241 SQTETHNVFVQEAKECNPEFERNVENTSCFMVPGVLPDLTNTVRIRVKTNKLCEYDDKL 300
Db 267 SQTETHNVFVQEAKECNPEFERNVENTSCFMVPGVLPDLTNTVRIRVKTNKLCEYDDKL 326
Qy 301 WSNWSQEMSGKGRNSTLYITMLLIYPVIVAGAIIVLLLYLKLKIIIFPPIDPGKIFK 360
Db 327 WSNWSQEMSGKGRNSTLYITMLLIYPVIVAGAIIVLLLYLKLKIIIFPPIDPGKIFK 386
Qy 361 EMFGDQNDTLHWKKYDIYEKQTKETSDSVLIENLKASQ 401
Db 387 EMFGDQNDTLHWKKYDIYEKQTKETSDSVLIENLKASQ 427

RESULT 2

US-11-067-251-3
; Sequence 3, Application US/11067251
; Publication No. US20050191730A1
; GENERAL INFORMATION:
; APPLICANT: Karow, Margaret
; APPLICANT: Fairhurst, Jeanette
; TITLE OF INVENTION: IL-4/IL-13 Specific Polypeptides and Therapeutic Uses Thereof
; FILE REFERENCE: 2020A
; CURRENT APPLICATION NUMBER: US/11/067,251
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 60/548,541
; PRIOR FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: 60/602,139
; PRIOR FILING DATE: 2004-08-17
; PRIOR APPLICATION NUMBER: 60/628,343
; PRIOR FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-067-251-3

Query Match 100.0%; Score 2172; DB 6; Length 427;
Best Local Similarity 100.0%; Pred. No. 7.8e-180;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTETOPPVTNLVSVENLCTVIWTWNPPEGASNSCLWYFSGDKQDKKIAPETRRI 60
Db 27 APTETOPPVTNLVSVENLCTVIWTWNPPEGASNSCLWYFSGDKQDKKIAPETRRI 86
Qy 61 EVPLNERICLVGSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120
Db 87 EVPLNERICLVGSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 146
Qy 121 LPRGNTSPDNTYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 180
Db 147 LPRGNTSPDNTYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 206
Qy 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNFISRCLFYEVVNN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNFISRCLFYEVVNN 266
Qy 241 SQTETHNVFVQEAKECNPEFERNVENTSCFMVPGVLPDLTNTVRIRVKTNKLCEYDDKL 300
Db 267 SQTETHNVFVQEAKECNPEFERNVENTSCFMVPGVLPDLTNTVRIRVKTNKLCEYDDKL 326

Qy 301 WSNWSQEMSGKGRNSTLYITMLLIYPVIVAGAIIVLLLYLKLKIIIFPPIDPGKIFK 360
Db 327 WSNWSQEMSGKGRNSTLYITMLLIYPVIVAGAIIVLLLYLKLKIIIFPPIDPGKIFK 386
Qy 361 EMFGDQNDTLHWKKYDIYEKQTKETSDSVLIENLKASQ 401
Db 387 EMFGDQNDTLHWKKYDIYEKQTKETSDSVLIENLKASQ 427

RESULT 3

US-10-850-270-4
; Sequence 4, Application US/10850270
; Publication No. US20050058645A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd (for all States except the US)
; APPLICANT: Dunlop, Felicity (US only)
; APPLICANT: Baca, Manuel (US only)
; APPLICANT: Nash, Andrew (US only)
; APPLICANT: Fabri, Louis (US only)
; TITLE OF INVENTION: Novel peptides
; FILE REFERENCE: 12175890/EJH
; CURRENT APPLICATION NUMBER: US/10/850,270
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: AU PS1301
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: AU 20039900437
; PRIOR FILING DATE: 2003-02-03
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 427
; TYPE: PRT
; ORGANISM: human
US-10-850-270-4

Query Match 99.7%; Score 2165; DB 5; Length 427;
Best Local Similarity 99.8%; Pred. No. 3.2e-179;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APTETOPPVTNLVSVENLCTVIWTWNPPEGASNSCLWYFSGDKQDKKIAPETRRI 60
Db 27 APTETOPPVTNLVSVENLCTVIWTWNPPEGASNSCLWYFSGDKQDKKIAPETRRI 86
Qy 61 EVPLNERICLVGSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120
Db 87 EVPLNERICLVGSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 146
Qy 121 LPRGNTSPDNTYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 180
Db 147 LPRGNTSPDNTYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 206
Qy 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNFISRCLFYEVVNN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNFISRCLFYEVVNN 266
Qy 241 SQTETHNVFVQEAKECNPEFERNVENTSCFMVPGVLPDLTNTVRIRVKTNKLCEYDDKL 300
Db 267 SQTETHNVFVQEAKECNPEFERNVENTSCFMVPGVLPDLTNTVRIRVKTNKLCEYDDKL 326
Qy 301 WSNWSQEMSGKGRNSTLYITMLLIYPVIVAGAIIVLLLYLKLKIIIFPPIDPGKIFK 360
Db 327 WSNWSQEMSGKGRNSTLYITMLLIYPVIVAGAIIVLLLYLKLKIIIFPPIDPGKIFK 386
Qy 361 EMFGDQNDTLHWKKYDIYEKQTKETSDSVLIENLKASQ 401
Db 387 EMFGDQNDTLHWKKYDIYEKQTKETSDSVLIENLKASQ 427

RESULT 4

US-10-036-568-4
; Sequence 4, Application US/10036568
; Publication No. US20020090682A1
; GENERAL INFORMATION:


```
; APPLICANT: Willson, Tracy
; APPLICANT: Nicola, Nicos A.
; APPLICANT: Hilton, Douglas J.
; APPLICANT: Metcalf, Donald
; APPLICANT: Zhang, Jian G.
; TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
; TITLE OF INVENTION: ENCODING SAME
; FILE REFERENCE: Davies cc
; CURRENT APPLICATION NUMBER: US/10/036,568
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US/09/051,843
; PRIOR FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Human IL-13 receptor alpha-chain
US-10-036-568-4

Query Match      99.2%; Score 2154; DB 4; Length 426;
Best Local Similarity 99.3%; Pred. No. 2.9e-178;
Matches 398; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRISI 60
Db 26 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRISI 85
Qy 61 EVPLNERICLVQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 120
Db 86 EVPLNERICLVQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 145
Qy 121 LPGNTSPDNTYLYWHRSLEKIHQCEINIPREGQYFGCSPDLTKVKQSSFEQHSVQIMV 180
Db 146 LPGNTSPDNTYLYWHRSLEKIHQCEINIPREGQYFGCSPDLTKVKQSSFEQHSVQIMV 205
Qy 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLVQWENPQNFISRCLFYEVEVNN 240
Db 206 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLVQWENPQNFISRCLFYEVEVNN 265
Qy 241 SQTETHNVFYVQEAKECENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYDDKL 300
Db 266 SQTETHNVFYVQEAKECENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYDDKL 325
Qy 301 WSNWSQEMSIKGNSTLYITMLLIVPVIVAGAIIVLLLYLKLKLIIFPPIDPGKIFK 360
Db 326 WSNWSQEMTIIVKGNSTLYITMLLIVPVIVAGAIIVLLLYLKLKLIIFPPIDPGKIFK 385
Qy 361 EMFGDQNDTLHWKXYDIYEKOTKEETDSVVLLENLKKASQ 401
Db 386 EMFGDQNDTLHWKXYDIYEKOTKEETDSVVLLENLKKASQ 426

RESULT 5
US-09-828-995B-50
; Sequence 50, Application US/09828995B
; Patent No. US20020165135A1
; GENERAL INFORMATION:
; APPLICANT: Heskia Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13 R
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/09/828,995B
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-753-159-50
Query Match      86.0%; Score 1869; DB 4; Length 405;
Best Local Similarity 85.5%; Pred. No. 1.5e-153;
Matches 343; Conservative 24; Mismatches 34; Indels 0; Gaps 0;

Qy 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRISI 60
Db 5 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRISK 64
Qy 61 EVPLNERICLVQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 120
Db 65 EVPLNERICLVQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCTW 124
; SEQ ID NO 50
; LENGTH: 405
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; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-828-995B-50

Query Match      86.0%; Score 1869; DB 3; Length 405;
Best Local Similarity 85.5%; Pred. No. 1.5e-153;
Matches 343; Conservative 24; Mismatches 34; Indels 0; Gaps 0;

Qy 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRISI 60
Db 5 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRISK 64
Qy 61 EVPLNERICLVQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 120
Db 65 EVPLNERICLVQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCTW 124
Qy 121 LPGNTSPDNTYLYWHRSLEKIHQCEINIPREGQYFGCSPDLTKVKQSSFEQHSVQIMV 180
Db 125 LPGNTSPDNTYLYWHRSLEKIHQCEINIPREGQYFGCSPDLTKVKQSSFEQHSVQIMV 184
Qy 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLVQWENPQNFISRCLFYEVEVNN 240
Db 185 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLVQWENPQNFISRCLFYEVEVNN 244
Qy 241 SQTETHNVFYVQEAKECENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYDDKL 300
Db 245 SQTETHNVFYVQEAKECENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYDDKL 304
Qy 301 WSNWSQEMSIKGNSTLYITMLLIVPVIVAGAIIVLLLYLKLKLIIFPPIDPGKIFK 360
Db 305 WSNWSQEMSIKGNSTLYITMLLIVPVIVAGAIIVLLLYLKLKLIIFPPIDPGKIFK 364
Qy 361 EMFGDQNDTLHWKXYDIYEKOTKEETDSVVLLENLKKASQ 401
Db 365 EMFGDQNDTLHWKXYDIYEKOTKEETDSVVLLENLKKASQ 405

RESULT 6
US-10-753-159-50
; Sequence 50, Application US/10753159
; Publication No. US20040142372A1
; GENERAL INFORMATION:
; APPLICANT: Heskia Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13 R
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/10/753,159
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-753-159-50
Query Match      86.0%; Score 1869; DB 4; Length 405;
Best Local Similarity 85.5%; Pred. No. 1.5e-153;
Matches 343; Conservative 24; Mismatches 34; Indels 0; Gaps 0;

Qy 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRISI 60
Db 5 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRISK 64
Qy 61 EVPLNERICLVQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 120
Db 65 EVPLNERICLVQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCTW 124
; SEQ ID NO 50
; LENGTH: 405
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QY 121 L PGRNTSPDNTYLYYHRSLEKIHOCEINIFREGQYFGCSFDLTWKVDSSFEQHSQIWMV 180
Db 125 L PGRNTSPDNTYLYYHRSLEKIHOCEINIFREGQYFGCSFDLTWKVDSSFEQHSQIWMV 184
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYQWENPQNFISRCIFYEVEVNN 240
Db 185 KDNARKIRPSFNIVPLTSRVKPPPHIKNLSFHNDDLYQWENPQNFISRCIFYEVEVNN 244
QY 241 SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDNTLVTRIRVTKNKLCEYDDKL 300
Db 245 SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDNTLVTRIRVTKNKLCEYDDKL 304
QY 301 WSNWSQEMSGKKNSTLYITMLLIVPVIVAGAILVLLLYLKLKIIIFPPIP 360
Db 305 WSNWSQEMSGKKNSTLYITMLLIVPVIVAGAILVLLLYLKLKIIIFPPIP 364
QY 361 EMFGDQNDTLHWKDYIYBKQKEETDSVVLJENLKKASQ 401
Db 365 EMFGDQNDTLHWKDYIYBKQKEETDSVVLJENLKKASQ 405
RESULT 7
US-10-850-270-10
; Sequence 10, Application US/10850270
; Publication No. US20050058645A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd (for all States except the US)
; APPLICANT: Dunlop, Felicity (US only)
; APPLICANT: Baca, Manuel (US only)
; APPLICANT: Nash, Andrew (US only)
; APPLICANT: Fabri, Louis (US only)
; TITLE OF INVENTION: Novel peptides
; FILE REFERENCE: 121/5890/EJH
; CURRENT APPLICATION NUMBER: US/10/850,270
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: AU PS1301
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: AU 2003900437
; PRIOR FILING DATE: 2003-02-03
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 664
; TYPE: PRT
; ORGANISM: human
US-10-850-270-10

Query Match 82.2%; Score 1784.5; DB 5; Length 664;
Best Local Similarity 91.7%; Pred. No. 6.5e-146;
Matches 333; Conservative 8; Mismatches 15; Indels 7; Gaps 3;
QY 1 APTETOPPVTNLVSVENLCTVIWTWNPPEGASNSCLWYFHFHFGDKQDKKIAPETRRSI 60
Db 45 APTETOPPVTNLVSVENLCTVIWTWNPPEGASNSCLWYFHFHFGDKQDKKIAPETRRSI 104
QY 61 EVPLNERICLVQSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120
Db 105 EVPLNERICLVQSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 164
QY 121 L PGRNTSPDNTYLYYHRSLEKIHOCEINIFREGQYFGCSFDLTWKVDSSFEQHSQIWMV 180
Db 165 L PGRNTSPDNTYLYYHRSLEKIHOCEINIFREGQYFGCSFDLTWKVDSSFEQHSQIWMV 224
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYQWENPQNFISRCIFYEVEVNN 240
Db 225 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYQWENPQNFISRCIFYEVEVNN 284
QY 241 SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDNTLVTRIRVTKNKLCEYDDKL 300
Db 285 SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDNTLVTRIRVTKNKLCEYDDKL 344
QY 301 WSNWSQEMSGKKNSTLYITMLLIVPVIVAGAILVLLLYLKLKIIIFPPIP 354

Db 345 WSNWSQEMSGKKNSTGEIE-AIVVPVCLAFLLTLLGLVLCFCNKEDLIKHIWPNVPD 403
QY 355 PGK 357
Db 404 PSK 406
RESULT 8
US-09-935-868-36
; Sequence 36, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-36
Query Match 80.6%; Score 1750; DB 3; Length 776;
Best Local Similarity 90.7%; Pred. No. 8e-143;
Matches 323; Conservative 5; Mismatches 14; Indels 14; Gaps 2;
QY 1 APTETOPPVTNLVSVENLCTVIWTWNPPEGASNSCLWYFHFHFGDKQDKKIAPETRRSI 60
Db 232 APTETOPPVTNLVSVENLCTVIWTWNPPEGASNSCLWYFHFHFGDKQDKKIAPETRRSI 291
QY 61 EVPLNERICLVQSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120
Db 292 EVPLNERICLVQSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 351
QY 121 L PGRNTSPDNTYLYYHRSLEKIHOCEINIFREGQYFGCSFDLTWKVDSSFEQHSQIWMV 180
Db 352 L PGRNTSPDNTYLYYHRSLEKIHOCEINIFREGQYFGCSFDLTWKVDSSFEQHSQIWMV 411
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYQWENPQNFISRCIFYEVEVNN 240
Db 412 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYQWENPQNFISRCIFYEVEVNN 471
QY 241 SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDNTLVTRIRVTKNKLCEYDDKL 300
Db 472 SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDNTLVTRIRVTKNKLCEYDDKL 531
QY 301 WSNWSQEMSGKKNST--LYITMLLIVPVIVAGAILVLLLYLKLKIIIFPPIP 353
Db 532 WSNWSQEMSGKKNSTGDKTHCTCPAPPELLGGP-----SVPLFPKP 576

RESULT 9
US-09-313-942-30
; Sequence 30, Application US/09313942
; Publication No. US20020012962A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-30

Query Match      80.5%; Score 1749.5; DB 3; Length 784;
Best Local Similarity 90.5%; Pred. No. 8.9e-143;
Matches 323; Conservative 5; Mismatches 14; Indels 15; Gaps 2;

Qy 1 APTETQPPVTNLSVSVENLCTVIWTPNPPEGASNCSLWYFSGDKQDKKIAPETRISI 60
Db 239 APTETQPPVTNLSVSVENLCTVIWTPNPPEGASNCSLWYFSGDKQDKKIAPETRISI 298
Qy 61 EVPLNERICLVQSGQCSNTESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 120
Db 299 EVPLNERICLVQSGQCSNTESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 358
Qy 121 LPRNTSPDNTYTLTYWHRSLKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSQVIMV 180
Db 359 LPRNTSPDNTYTLTYWHRSLKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSQVIMV 418
Qy 181 KDNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFNHDDLIVQWENPQNFISRCLFYEVVNN 240
Db 419 KDNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFNHDDLIVQWENPQNFISRCLFYEVVNN 478
Qy 241 SQTETHNVFVYQAEKACENPEFERNVENTSCFMVPGVLPDNTLTVIRVKTNKLKYEDDKL 300
Db 479 SQTETHNVFVYQAEKACENPEFERNVENTSCFMVPGVLPDNTLTVIRVKTNKLKYEDDKL 538
Qy 301 WSNWSQEMSIGKRNST-----LYITMLLIIVPVIIVAGAIIVLLLYLKLKLIIFPPIP 353
Db 539 WSNWSQEMSIGKRNSTGDKTHTCCPCPAPELLGGP-----SVFLFPPKP 584

RESULT 10
US-09-935-868-30
; Sequence 30, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-30

Query Match      80.5%; Score 1749.5; DB 3; Length 784;
Best Local Similarity 90.5%; Pred. No. 8.9e-143;
Matches 323; Conservative 5; Mismatches 14; Indels 15; Gaps 2;

Qy 1 APTETQPPVTNLSVSVENLCTVIWTPNPPEGASNCSLWYFSGDKQDKKIAPETRISI 60
Db 239 APTETQPPVTNLSVSVENLCTVIWTPNPPEGASNCSLWYFSGDKQDKKIAPETRISI 298
Qy 61 EVPLNERICLVQSGQCSNTESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 120
Db 299 EVPLNERICLVQSGQCSNTESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 358
Qy 121 LPRNTSPDNTYTLTYWHRSLKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSQVIMV 180
Db 359 LPRNTSPDNTYTLTYWHRSLKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSQVIMV 418
Qy 181 KDNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFNHDDLIVQWENPQNFISRCLFYEVVNN 240
Db 419 KDNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFNHDDLIVQWENPQNFISRCLFYEVVNN 478
Qy 241 SQTETHNVFVYQAEKACENPEFERNVENTSCFMVPGVLPDNTLTVIRVKTNKLKYEDDKL 300
Db 479 SQTETHNVFVYQAEKACENPEFERNVENTSCFMVPGVLPDNTLTVIRVKTNKLKYEDDKL 538
Qy 301 WSNWSQEMSIGKRNST-----LYITMLLIIVPVIIVAGAIIVLLLYLKLKLIIFPPIP 353
Db 539 WSNWSQEMSIGKRNSTGDKTHTCCPCPAPELLGGP-----SVFLFPPKP 584

RESULT 11
US-10-287-035-30
; Sequence 30, Application US/10287035
; Publication No. US20030104567A1
; GENERAL INFORMATION:
; APPLICANT: Neil Stahl and George D. Yancopoulos
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203DA
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US/10/287,035
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: USSN 09/935,868
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: USSN 09/787,835
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-035-30

Query Match      80.5%; Score 1749.5; DB 4; Length 784;
Best Local Similarity 90.5%; Pred. No. 8.9e-143;
Matches 323; Conservative 5; Mismatches 14; Indels 15; Gaps 2;

Qy 1 APTETQPPVTNLSVSVENLCTVIWTPNPPEGASNCSLWYFSGDKQDKKIAPETRISI 60
Db 239 APTETQPPVTNLSVSVENLCTVIWTPNPPEGASNCSLWYFSGDKQDKKIAPETRISI 298
Qy 61 EVPLNERICLVQSGQCSNTESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 120
Db 299 EVPLNERICLVQSGQCSNTESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 358
Qy 121 LPRNTSPDNTYTLTYWHRSLKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSQVIMV 180
Db 359 LPRNTSPDNTYTLTYWHRSLKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSQVIMV 418
Qy 181 KDNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFNHDDLIVQWENPQNFISRCLFYEVVNN 240
Db 419 KDNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFNHDDLIVQWENPQNFISRCLFYEVVNN 478
Qy 241 SQTETHNVFVYQAEKACENPEFERNVENTSCFMVPGVLPDNTLTVIRVKTNKLKYEDDKL 300
Db 479 SQTETHNVFVYQAEKACENPEFERNVENTSCFMVPGVLPDNTLTVIRVKTNKLKYEDDKL 538
Qy 301 WSNWSQEMSIGKRNST-----LYITMLLIIVPVIIVAGAIIVLLLYLKLKLIIFPPIP 353
Db 539 WSNWSQEMSIGKRNSTGDKTHTCCPCPAPELLGGP-----SVFLFPPKP 584

RESULT 12
US-10-282-162-30
; Sequence 30, Application US/10282162
; Publication No. US20030143697A1
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; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: 2003-09-22
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-30

Query Match      80.5%; Score 1749.5; DB 4; Length 784;
Best Local Similarity 90.5%; Pred. No. 8.9e-143;
Matches 323; Conservative 5; Mismatches 14; Indels 15; Gaps 2;

QY 1 APTETOPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 60
Db 239 APTETOPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 298
QY 61 EYPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 120
Db 299 EYPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 358
QY 121 LPCRNTSPDNTNYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSQIWMV 180
Db 359 LPCRNTSPDNTNYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSQIWMV 418
QY 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKNLSFHNDLLYQWENPQNFISRCIFYEVEVNN 240
Db 419 KDNAGKIKPSFNIVPLTSRVKPDPPHINKNLSFHNDLLYQWENPQNFISRCIFYEVEVNN 478
QY 241 SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYDDKL 300
Db 479 SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYDDKL 538
QY 301 WSNWSQEMSIGKRNST----LYITMLLIVPVIVAGAIIVLLLYLRLKLIIPPPIP 353
Db 539 WSNWSQEMSIGKRNSTTGDKTHTCCPAPPELLGGP-----SVFLFPPKP 584

RESULT 13
US-11-134-114-30
; Sequence 30, Application US/11/134,114
; Publication No. US2005022033A1
; GENERAL INFORMATION:
; APPLICANT: Stahl, Neil
; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: Receptor Based Antagonists and Methods of Making and Using
; FILE REFERENCE: 2003C1
; CURRENT APPLICATION NUMBER: US/11/134,114
; CURRENT FILING DATE: 2005-05-20
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-114-30

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Best Local Similarity 90.5%; Pred. No. 8.9e-143;
Matches 323; Conservative 5; Mismatches 14; Indels 15; Gaps 2;

QY 1 APTETOPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 60
Db 239 APTETOPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 298
QY 61 EYPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 120
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QY 121 LPCRNTSPDNTNYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSQIWMV 180
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Db 419 KDNAGKIKPSFNIVPLTSRVKPDPPHINKNLSFHNDLLYQWENPQNFISRCIFYEVEVNN 478
QY 241 SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYDDKL 300
Db 479 SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYDDKL 538
QY 301 WSNWSQEMSIGKRNST----LYITMLLIVPVIVAGAIIVLLLYLRLKLIIPPPIP 353
Db 539 WSNWSQEMSIGKRNSTTGDKTHTCCPAPPELLGGP-----SVFLFPPKP 584

RESULT 14
US-09-825-561A-82
; Sequence 82, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677A1ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-82

Query Match      80.3%; Score 1745; DB 3; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.6e-143;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 6 APTETOPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 65
QY 61 EYPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 120
Db 66 EYPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 125
QY 121 LPCRNTSPDNTNYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSQIWMV 180
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Db 126 LFGRTSPDNTYLLYWHRSLEKIHQENIFREGQYFGCSFDLTAKVDSSFEQHSVQIMV 185
Qy 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDDLYVQWENPQNFISRCLFYEVVNN 240
Db 186 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDDLYVQWENPQNFISRCLFYEVVNN 245
Qy 241 SQTETHNVFYVQEAACENPEFERNVENTSCFMVPGVLPDNLNTVIRVKTNKLCEYDDKL 300
Db 246 SQTETHNVFYVQEAACENPEFERNVENTSCFMVPGVLPDNLNTVIRVKTNKLCEYDDKL 305
Qy 301 WSNWSQEMSIGKKRNST 317
Db 306 WSNWSQEMSIGKKRNST 322
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RESULT 15

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US-10-872-087-82
; Sequence 82, Application US/10872087
; Publication No. US20040235743A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Novak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHAL1 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22D1
; CURRENT APPLICATION NUMBER: US/10/872,087
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 09/825,561
; PRIOR FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-087-82
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Query Match 80.3%; Score 1745; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.6e-143;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFQDKODKKIAPETRSI 60
Db 6 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFQDKODKKIAPETRSI 65
Qy 61 EVDPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPPEASVTELCIWHNLSYMKCSW 120
Db 66 EVDPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPPEASVTELCIWHNLSYMKCSW 125
Qy 121 LFGRTSPDNTYLLYWHRSLEKIHQENIFREGQYFGCSFDLTAKVDSSFEQHSVQIMV 180
Db 126 LFGRTSPDNTYLLYWHRSLEKIHQENIFREGQYFGCSFDLTAKVDSSFEQHSVQIMV 185
Qy 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDDLYVQWENPQNFISRCLFYEVVNN 240
Db 186 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDDLYVQWENPQNFISRCLFYEVVNN 245
Qy 241 SQTETHNVFYVQEAACENPEFERNVENTSCFMVPGVLPDNLNTVIRVKTNKLCEYDDKL 300
Db 246 SQTETHNVFYVQEAACENPEFERNVENTSCFMVPGVLPDNLNTVIRVKTNKLCEYDDKL 305
Qy 301 WSNWSQEMSIGKKRNST 317
Db 306 WSNWSQEMSIGKKRNST 322
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 22:29:50 ; Search time 8.74019 Seconds
(without alignments)
602.062 Million cell updates/sec

Title: US-10-036-568A-4_COPY_26_426

Perfect score: 2172

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB_PEP.*
- 2: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB_PEP.*
- 3: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB_PEP.*
- 4: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB_PEP.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2172	100.0	427	US-11-185-230-4	Sequence 4, Appli
2	1679.5	77.3	424	US-11-185-230-6	Sequence 6, Appli
3	296.5	13.7	420	US-11-185-230-5	Sequence 5, Appli
4	294.5	13.6	380	US-10-989-313-4	Sequence 4, Appli
5	294.5	13.6	380	US-11-185-230-2	Sequence 2, Appli
6	293.5	13.5	378	US-11-185	Sequence 12, Appli
7	287.5	13.2	383	US-10-989-313-2	Sequence 2, Appli
8	230	10.6	313	US-11-193-512-106	Sequence 106, App
9	202	9.3	341	US-10-511-722-21	Sequence 21, Appli
10	202	9.3	357	US-10-511-722-20	Sequence 20, Appli
11	202	9.3	369	US-11-105-268-60	Sequence 60, Appli
12	178.5	8.2	411	US-11-075-351-47	Sequence 47, Appli
13	173	8.0	646	US-10-995-561-695	Sequence 695, App
14	173	8.0	708	US-10-636-320-2	Sequence 2, Appli
15	173	8.0	918	US-10-995-561-696	Sequence 696, App
16	168.5	7.8	329	US-10-995-561-694	Sequence 694, App
17	168	7.7	897	US-11-124-367A-449	Sequence 449, App
18	168	7.7	897	US-11-124-367A-451	Sequence 451, App
19	166	7.6	903	US-11-124-367A-450	Sequence 450, App
20	125	5.8	825	US-10-995-561-679	Sequence 679, App
21	125	5.8	825	US-11-124-367A-469	Sequence 469, App
22	125	5.8	852	US-11-104-923A-5	Sequence 5, Appli
23	113	5.2	631	US-10-813-646-22	Sequence 22, Appli
24	111.5	5.1	979	US-10-636-320-6	Sequence 6, Appli
25	107.5	4.9	360	US-11-084-408-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-11-185-230-4
; Sequence 4, Application US/11185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vitca, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 427
; TYPE: PRT 3
; ORGANISM: Homo sapiens
; FEATURE:
US-11-185-230-4

Query Match	100.0%	Score 2172;	DB 7;	Length 427;
Best Local Similarity	100.0%	Pred. No. 2.3e-184;		
Matches 401;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	APTETQPPVTNLVSVENLCTVITWNPPEGASNCISLWYFSHFQDKQDKKIAPETRISI	60	
DB	27	APTETQPPVTNLVSVENLCTVITWNPPEGASNCISLWYFSHFQDKQDKKIAPETRISI	86	
QY	61	EVPLNERICLVGSCQCSNESEKPSILVEKISPEGDPESAVTELCIWHNLSYMKCSW	120	
DB	87	EVPLNERICLVGSCQCSNESEKPSILVEKISPEGDPESAVTELCIWHNLSYMKCSW	146	
QY	121	LPGRNTSPDTNTLYYHRSLEKIHOCENIFREGYFGCSFDLTVKVDSSEFQHSVQIMV	180	
DB	147	LPGRNTSPDTNTLYYHRSLEKIHOCENIFREGYFGCSFDLTVKVDSSEFQHSVQIMV	206	
QY	181	KDNAGIKPSPNIVPLTSRVKPDPPHINKLSFNHNDLTVQWENPNQFISRCLFYEVVNN	240	
DB	207	KDNAGIKPSPNIVPLTSRVKPDPPHINKLSFNHNDLTVQWENPNQFISRCLFYEVVNN	266	
QY	241	SQTETHNVFYVQEAACENPEFERNVENTSCFMPVGLPDTLNTVIRVTKNLCYEDDKL	300	
DB	267	SQTETHNVFYVQEAACENPEFERNVENTSCFMPVGLPDTLNTVIRVTKNLCYEDDKL	326	

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QY 301 WSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLLKIIIFPPIDPGKIFK 360
Db 327 WSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLLKIIIFPPIDPGKIFK 386
QY 361 EMFGDQNDTLHWKKYDIYKQTKETSDSVLLIENLKASQ 401
Db 387 EMFGDQNDTLHWKKYDIYKQTKETSDSVLLIENLKASQ 427

RESULT 2
US-11-185-230-6
; Sequence 6, Application US/11185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; PRIOR FILING DATE: 2005-07-18
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 424
; TYPE: PRT 3
; ORGANISM: Mus musculus
; FEATURE:
US-11-185-230-6

Query Match 77.3%; Score 1679.5; DB 7; Length 424;
Best Local Similarity 77.0%; Pred. No. 6.9e-141;
Matches 308; Conservative 40; Mismatches 51; Indels 1; Gaps 1;

QY 1 APTETQPPVNLVSVENLCTVIWTWNPPEGASNCSLWYFHFQDKQDKKIAPETRISI 60
Db 25 AATEVQPPVNLVSVENLCTVIWTWNPPEGASPNCTLYFHFQDKQDKKIAPETRISKE 84
QY 61 EVPLNERICLVQSCSTNESEKPSILVEKICIPPEGDPESAVTELQCIWHNLSYMKCSW 120
Db 85 ELPLDEKICLVQSCSTNESEKPSILVEKICIPPEGDPESAVTELQCIWHNLSYMKCSW 144
QY 121 LQGRNTSPDNTLYLYWHRSLKIHQCNIFREGQYFGCSFDLTWKVDSSEFQHSQIMV 180
Db 145 LQGRNTSPDNTLYLYWHRSLKIHQCNIFREGQYFGCSFDLTWKVDSSEFQHSQIMV 203
QY 181 KDNAGKIPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNPISRLCYFEVEVNN 240
Db 204 KDNAGKIPSKIVSLTSYVVKPPPHIKNLSFHNDDLYVQWENPQNPISRLCYFEVEVNN 263
QY 241 SQTEHNVFVQAKCNPFERNVENTSCFVMPGVLPDNTLVTRVKTNKLCEYEDKL 300
Db 264 TQDRHNLVEEDKCNSEDRNMGTSQFLPGVLADAVYTRVRVKTNKLCEYEDKL 323
QY 301 WSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLLKIIIFPPIDPGKIFK 360
Db 324 WSDWSEASQISGKSNSTFYTTMLLTIPFVAVAVIILLFYLKRLKIIIFPPIDPGKIFK 383
QY 361 EMFGDQNDTLHWKKYDIYKQTKETSDSVLLIENLKAS 400
Db 384 EMFGDQNDTLHWKKYDIYKQTKETSDSVLLIENLKAA 423

RESULT 3
US-11-185-230-5
; Sequence 5, Application US/11185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
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; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 420
; TYPE: PRT 3
; ORGANISM: Homo sapiens
; FEATURE:
US-11-185-230-5

Query Match 13.7%; Score 296.5; DB 7; Length 420;
Best Local Similarity 24.8%; Pred. No. 8.5e-19;
Matches 102; Conservative 65; Mismatches 180; Indels 65; Gaps 16;

QY 7 PPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFHFQDKQDKKIAPETRISIEVPLN 65
Db 32 PPV-NFTIKVTGLAQVLLQWKNPDQQRNVNLEY-----QVKINAPK-EDDYETRI 82
QY 66 ERICLVQ-----GSCQSTNESEKPSILVEKICIS-----PPEGDPESAVTELQCIWHNL--- 113
Db 83 ESKCVTILHKGFSAVRITILQNDHSLASSWASAEHLHAPGSPGTSIVNLCTCTTTNTE 142
QY 114 -----SY-----MKCSWLPGRNTSPDNTLYLYWHRSLKIHQCNIPRE--GOYFGCSFDL 163
Db 143 YSLRSTYQSLHCTWLVGTDAPEDTQYFLYRYGSWTE--ECQYKDTLGRNIACWFR 200
QY 164 TKVDSSEFQHSQIMVQKONAGKIPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWEN 223
Db 201 TPILSKGRDWLSVLVNGSSKHSARPPDQLFALHAIQINPLNPLVTAIEIGTRLSIQWEK 260
QY 224 PQN-FISRLCYFEVEVNNQSTETHNVFYVQEAECENPEFERNVENTSCFVMPGVLPDTLN 282
Db 261 PVSAPFIFCHDFYEVKIHNTNRG-----YLQIEKLMTNAFISIIDLSKY----- 304
QY 283 TVRIRVKTNKLCEYEDDKLMSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLLYLK 342
Db 305 DVQVRAAVSMCREAG-LWSEWSQPIVGVNDEKHPKREWFVIVIMATICIFILILSLICK 363
QY 343 --RLKIIIFPPIDPGKIFKEMFGDQNDTLHWKKYDIYKQTKETSDSVL 392
Db 364 ICHLWIKLFPPIAPKSNIKDLFVTTN-----YEKAGSSETEIEVI 404

RESULT 4
US-10-989-313-4
; Sequence 4, Application US/10989313
; Publication No. US20050277126A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lora
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; APPLICANT: Wills-Karp, Marsha
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: Cytokine Receptor Chain
; FILE REFERENCE: GI 5268A
; CURRENT APPLICATION NUMBER: US/10/989,313
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US/09/868,123
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 380
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Publication No. US20050287144A1	
GENERAL INFORMATION:	
APPLICANT: Yeda Research and Development Co. Ltd.	
APPLICANT: Wallach, David	
APPLICANT: Shmushkovich, Taisia	
APPLICANT: Ramakrishnan, Parameswaran	
TITLE OF INVENTION: Derivatives of the IL-2 receptor Gamma chain, their preparation a	
FILE REFERENCE: 530	
CURRENT APPLICATION NUMBER: US/10/511,722	
PRIOR FILING DATE: 2004-10-18	
PRIOR APPLICATION NUMBER: 149217	
PRIOR FILING DATE: 2002-04-18	
PRIOR APPLICATION NUMBER: 152183	
PRIOR FILING DATE: 2002-10-08	
NUMBER OF SEQ ID NOS: 21	
SOFTWARE: Patent in version 3.1	
SEQ ID NO 21	
LENGTH: 341	
TYPE: PRT	
ORGANISM: Homo sapiens	
US-10-511-722-21	
Query Match	
Best Local Similarity 9.3%; Score 202; DB 6; Length 341;	
Matches 72; Conservative 44; Mismatches 101; Indels 48; Gaps 14;	
Qy	105 ELQCIWNLNLSYMKCSWLPGRNTSPDTNLTYYWHRSL--EKIHOCEN-IFREGQYFGCSF 161
Db	59 EVQCFVFNVEYMNCTWNSSEPPQ--TNLTLYHYWYKNSDNDKVQKSHYLFSEETSGC-- 115
Qy	162 DLTKVKDSSFEQHSVQIMVKDNAGKIPSFNIVPLTSRVKDPDPHKKLSFH---NDDLY 218
Db	116 QLQKKEIHLVQTFVVQL--QDPREPRQATQMLKQLNLVIPWAP--ENLTLLKLSQLE 171
Qy	219 VQWENPQNFIISRCI-----FYEVVNNQSQTETHNVFYVQEAECENPEPERNVNENTSCFMVP 274
Db	172 LNNWN--RFLNHCLEHLVQYRTDWDHWT-----EQSVVYRHKFSLP 211
Qy	275 GVLPDPTLNTVIRVKTNKLCEYDDKLSNWSQMSIG---KRNSTLYITMLLIVPVIVA 331
Db	212 SVDGQKRYTFRVRSRFPNPLC-GSAQHWSEWSHPHWSGNTSKENPFLFALEAVVISVSGM 270
Qy	332 GAIIVLL---LYLKLKLIIFPPIP 353
Db	271 GLIISLLCVYFWLER-----TWPRIP 291
RESULT 11	
US-11-105-268-60	
Sequence 60, Application US/11105268	
Publication No. US20050260204A1	
GENERAL INFORMATION:	
APPLICANT: Allan, Christian	
TITLE OF INVENTION: ANTI-IL-9 ANTIBODY FORMULATIONS AND USES THEREOF	
FILE REFERENCE: 10271-126-999	
CURRENT APPLICATION NUMBER: US/11/105,268	
CURRENT FILING DATE: 2005-04-12	
PRIOR APPLICATION NUMBER: 60/561,845	
PRIOR FILING DATE: 2004-04-12	
NUMBER OF SEQ ID NOS: 60	
SOFTWARE: Patent in version 3.2	
SEQ ID NO 60	
LENGTH: 369	
TYPE: PRT	
ORGANISM: Homo sapiens	
US-11-105-268-60	
Query Match	
Best Local Similarity 9.3%; Score 202; DB 7; Length 369;	
Matches 72; Conservative 44; Mismatches 101; Indels 48; Gaps 14;	
Qy	105 ELQCIWNLNLSYMKCSWLPGRNTSPDTNLTYYWHRSL--EKIHOCEN-IFREGQYFGCSF 161
Db	59 EVQCFVFNVEYMNCTWNSSEPPQ--TNLTLYHYWYKNSDNDKVQKSHYLFSEETSGC-- 115
Qy	162 DLTKVKDSSFEQHSVQIMVKDNAGKIPSFNIVPLTSRVKDPDPHKKLSFH---NDDLY 218
Db	116 QLQKKEIHLVQTFVVQL--QDPREPRQATQMLKQLNLVIPWAP--ENLTLLKLSQLE 171
Qy	219 VQWENPQNFIISRCI-----FYEVVNNQSQTETHNVFYVQEAECENPEPERNVNENTSCFMVP 274
Db	172 LNNWN--RFLNHCLEHLVQYRTDWDHWT-----EQSVVYRHKFSLP 211
Qy	275 GVLPDPTLNTVIRVKTNKLCEYDDKLSNWSQMSIG---KRNSTLYITMLLIVPVIVA 331
Db	212 SVDGQKRYTFRVRSRFPNPLC-GSAQHWSEWSHPHWSGNTSKENPFLFALEAVVISVSGM 270
Qy	332 GAIIVLL---LYLKLKLIIFPPIP 353
Db	271 GLIISLLCVYFWLER-----TWPRIP 291
RESULT 12	
US-11-075-351-47	
Sequence 47, Application US/11075351	
Publication No. US20050260716A1	
Query Match	
Best Local Similarity 9.3%; Score 202; DB 6; Length 357;	
Matches 72; Conservative 44; Mismatches 101; Indels 48; Gaps 14;	
Qy	105 ELQCIWNLNLSYMKCSWLPGRNTSPDTNLTYYWHRSL--EKIHOCEN-IFREGQYFGCSF 161
Db	59 EVQCFVFNVEYMNCTWNSSEPPQ--TNLTLYHYWYKNSDNDKVQKSHYLFSEETSGC-- 115
Qy	162 DLTKVKDSSFEQHSVQIMVKDNAGKIPSFNIVPLTSRVKDPDPHKKLSFH---NDDLY 218
Db	116 QLQKKEIHLVQTFVVQL--QDPREPRQATQMLKQLNLVIPWAP--ENLTLLKLSQLE 171
Qy	219 VQWENPQNFIISRCI-----FYEVVNNQSQTETHNVFYVQEAECENPEPERNVNENTSCFMVP 274
Db	172 LNNWN--RFLNHCLEHLVQYRTDWDHWT-----EQSVVYRHKFSLP 211
Qy	275 GVLPDPTLNTVIRVKTNKLCEYDDKLSNWSQMSIG---KRNSTLYITMLLIVPVIVA 331
Db	212 SVDGQKRYTFRVRSRFPNPLC-GSAQHWSEWSHPHWSGNTSKENPFLFALEAVVISVSGM 270
Qy	332 GAIIVLL---LYLKLKLIIFPPIP 353
Db	271 GLIISLLCVYFWLER-----TWPRIP 291

Query Match 8.0%; Score 173; DB 6; Length 708;
Best Local Similarity 25.0%; Pred. No. 1.3e-07;
Matches 101; Conservative 51; Mismatches 194; Indels 58; Gaps 21;

QY 6 QPPVNLVSVENLCTVIWTWNPPEGASSNCSLWYFHFSG-DKQDKKIAPETRRSIEVPL 64
DB ESPVQLHSNFTAVCVLKEKCMYDFHVNAVIVWKTNHFTIPKEQYTIINRTASSVTFTD 93

QY 65 NERICLQVGSQCSTNESEKPSILVEKICIS--PPEGDPESAVTELOCIWHNLSYMKCSWLP 122
DB IASLNIQLTCNLTFCQLEQNVGITIISGLPPE-KPKN----LSCI VNEGKKMRCCEWDG 148

QY 123 GRNTSPDNTYTL--YYWHRSLEKIHOCENIFREGQYFGCSFDLTVKYKDSFQHSVQIMVK 181
DB GRETHLETNFTLKSEW--ATHKPADCK--AKRDTPTCTVDYSTV--YFVNIEVWVEAE 201

QY 182 DNAGKI-KPSFNIVPLTSRVPDPPIKHLNFHND--LYVOWENPQNFISRCLFYE 235
DB 202 NALGKVTSDHINFDPV-YKVKPNPH--NLSVINSEELSSILKLTWTPNPSIKSVIILKYN 258

QY 236 VEVNNSQETHTNFFVQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVTRIRVKNKLCY 295
DB 259 IQYRTKDASTWS-----QIPP-EDTASTRSSFTVQDLKPFTYVFRIR-----CM 302

QY 296 EDD--KLWSNWSQEMS--IGKRNSTLYITMLLIVPVIVAGAIIVLLLYLKLKLIIPPP 351
DB 303 KEDGKYMSDSEASGITYEDRPSKAPSFWKIDPSHTQGYRTVQLVW-KTL-----PP 356

QY 352 IPDPGKIFKEMFGDQNDTLLHWKKYDIYEKOTKEETSDSVVLIN 395
DB 357 FEANGKIL-----DYEVTLTRWKSH--LQNTVTVNATKLTVNLTN 393

RESULT 15

US-10-995-561-696
; Sequence 696, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 696
; LENGTH: 918
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-696

Query Match 8.0%; Score 173; DB 6; Length 918;
Best Local Similarity 25.0%; Pred. No. 1.8e-07;
Matches 101; Conservative 51; Mismatches 194; Indels 58; Gaps 21;

QY 6 QPPVNLVSVENLCTVIWTWNPPEGASSNCSLWYFHFSG-DKQDKKIAPETRRSIEVPL 64
DB ESPVQLHSNFTAVCVLKEKCMYDFHVNAVIVWKTNHFTIPKEQYTIINRTASSVTFTD 93

QY 65 NERICLQVGSQCSTNESEKPSILVEKICIS--PPEGDPESAVTELOCIWHNLSYMKCSWLP 122
DB IASLNIQLTCNLTFCQLEQNVGITIISGLPPE-KPKN----LSCI VNEGKKMRCCEWDG 148

QY 123 GRNTSPDNTYTL--YYWHRSLEKIHOCENIFREGQYFGCSFDLTVKYKDSFQHSVQIMVK 181
DB 149 GRETHLETNFTLKSEW--ATHKPADCK--AKRDTPTCTVDYSTV--YFVNIEVWVEAE 201

QY 182 DNAGKI-KPSFNIVPLTSRVPDPPIKHLNFHND--LYVOWENPQNFISRCLFYE 235
DB 202 NALGKVTSDHINFDPV-YKVKPNPH--NLSVINSEELSSILKLTWTPNPSIKSVIILKYN 258

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